

Figure 1

CGAGAGACGACAGAAGGTACGGCTGCGAGAACGACAGAACAGGGTCCAGAAAAA  
 GGAAAGTGTGGAGGGAGTGGGGACAAAAGCAGCGACCAAGTGAATGTCACCTC  
 AGTGAATGAGGCCAGGCACAAACGCGCGGAAGGATTGTGTAGCTGGGACCCCT  
 TCATAGACACTGATGACACGTTACGAAAATAGAAATTGAGGAGAACGCCCTGG  
 GCCTCGGAAAGGAGTGATTGATTAGTACTTGAAGTTAGGTGACTTTAACGGAGAA  
 CTAACATAATGTATACTATTGAGGGAGGAGGAAGGAGCATTACAGAGTTCCAGCAGC  
 AGCAGGAAAGCTTGGTTAATTGAAATGGATGATAGCATTAAAATAACAGAACGC  
 GCCTCCAGGTCTGAAGCTTCAGTCCCCAGCTGAAAGCCAGAAAAGACTAACAGC  
 CACTAACGCTTTGATCCCTTGGAGCAAAGAACCTTCCTCCCTGGGTGAAGAC  
 TCTCCTCAGAACGATTTCCTGTCCTGCCTATGTTACAAGAGGAATCAAACCAAGAC  
 AGAAGAGCTCAGGATGCAAGGTGAGAGGCAGGGAAAGTCAGCGGTTGATCTCCC  
 TCACTGCTGCTGCCTGGTCACCCCTGGGAGCAGGGCTGTCCTGCCGCTGTG  
 CCTGCTATGTGCCACAGAGGTGCACTGTACATTGGTACCTGACCTCCATCCCAG  
 ATGGCATCCCAGGCAATGTGAAACGAATAAATTAGGATATAACAGCCTACTAGAT  
 TGACAGAAAACGACTTGATGGCCTGAGCAAACCTGGAGTTACTCATGCTGACAGT  
 AATGGCATTACAGAGTCAGTGACAAGACCTCTCGGGCTTGCACTGCCAGGTC  
 TTAAAAATGAGCTATAACAAAGTCAAATCATTGGAGGATACTTCTACGGACTC  
 GGGAGCTGGTCCGGTGCACCTGGATCACAACAAATTGAATTCAACCCCTGAG  
 GCCTTATGGACTACCTCGCTCCGCTGGTACATTAGAACGGAAACCGGCTCACA  
 AAGCTCCATCCAGACACATTGTCTCATTAAGCTATCTCCAGATATTAAAACCTTT  
 TCATTAAGTACCTGTTCTGTCGATAACTTCCCTGACCTCCCTCCAAAAGAAATGGT  
 CTCCTACATGCCAACCTAGAAAGCCTGTATTGCAATGGAAACCCATGGACCTGTGA  
 CTGCCATTAAAGTGGTGTGAGTGGATGCAGGGAAACCCAGATATAATAAAAAT  
 GCAAGAAAGACAGAACGCTTCCAGTCAGCAATGTCCCCTTGCAATGAACCCCA  
 GGATCTCTAAAGGCAGACCCCTTGCTATGGTACCATCTGGAGCTTCTATGTACAA  
 AGCCAACCATTGATCCATCACTGAAGTCAAAGAGCCTGGTACTCAGGAGGACAAT  
 GGATCTGCCTCCACCTCACCTCAAGATTGATAGAACCCCTTGGCTCTGTCTTGA  
 ACATGACANANNTNTGGAAATAAGGCCGACATGGTCTGTAGTATCCAAAAGCCA  
 TCAAGGACATCACCACACTGCAATTGCAAGAAAATGACTACATCATGCTAAATGC  
 GTCATTTCACAAATCTGTGTGCACTGTAGATTATAATCACATCCAGCCAGTGTG  
 GCAACTCTGGCTTATACAGTGACTCTCTGTGATACTAGAACAGGAGCTTCTAGGCTGAAGA  
 TACCGAGACTCCTCACTGTCTTAGATATAAACAGGTGGCTTCTAGGCTGAAGA  
 CATTTTACCAAGCATAGAGGCTGATGTCAGAGCAGACCCCTTGGTCCAACAAGA  
 AAAAATTGTCTGCACTGAACAGAACCTGACCCACACTAGCACATTACAGATCCA  
 GTTTCCACTGATGCTCAAATCGCTTACCAAGGGCGGAGATGAGAGCGGAGAGAC  
 TCAAATGGACCATGATCCTGATGATGAAACAATCCAAACTGGAACGCACGTGCTGG  
 TTGGCGGCACTATTGCCCTGAGCTGTCCAGGCAAAGGCGACCCCTCACCTCACITGG  
 AATGGCTCTAGCTGATGGGAGTAAAGTGAAGAGGCCCTACGTTAGCGAGGATGGG

CGAATCTTAATAGACAAAATGGGAAGTGGAACTGCAGATGGCTGACAGCFTTGA  
 TGCAGGTCTTACCACTGCATAAGCACCAATGATGCAGATGCGGATGTTCTCACATA  
 CAGGATAACTGTGGTAGAGCCCTATGGAGAAAGCACACATGACAGTGGAGTCCAGC  
 ACACAGTGGITACGGGTGAGACGCTCGACCTTCATGCCTTCCACGGGTGTTCCAG  
 ATGCTTCTATTAGCTGGATTCTCCAGGGAACACTGTGTTCTCAGCCATCAAGAG  
 ACAGGCAAATTCTAACATGGACCTAACAGAATATTACAGGTACGCCAAAAGAT  
 CAAGGTCAATTACCAATGTGTGGCTGCCAACCCATCAGGGGCCACTTTCCAGTTT  
 AAAGTTCAAGTCAAAAGAAAGGCCAAGGATGGTGAGCATGACAGGGAGGCAG  
 GTGGATCTGGACTTGGAGAACCCAACCTCCAGTGTTCCTAACAGCAGCCAGCATCTT  
 TGAAACTCTGCATCAGCTTGACAGGGTCAGAGGCTGGAAAACAAGTCTCCGGTG  
 TACATAGGAAGAACAAACATAGAGACTAACATACATCGGCGCGTGGGATTCCACG  
 CTCCGGCGATTCAAGGGAGCATAGGAGGCAGCTCCCTCTCTGCTCGGAGAATTGAC  
 CCGCAACGCTGGCAGCACTCTAGAAAAAGCCAAAAGAATTCTGTGCCAAAAAAA  
 GCAAGAAAATACCACAGTAAAGCCAGTGCCTGGCATGATTCTCCAGATGAAGAAATTCA  
 CTGACGAGGAAAAGGATGCCTCTGGCATGATTCTCCAGATGAAGAAATTCA  
 TGAAAACTAAGGCTCTGGTGTCCCAGAAGGTACCAACTGCTGACTCTGGACCAG  
 TAAATCATGGTTTATGACGAGTATAGCTCTGGCACAGAAGTCTCAACTGTGAATC  
 CACAAACACTACAATCTGAGCACCTCCTGATTCAAATTATTAGTGTAAACAAACG  
 GTACAGCTGTGACAAGAGTATGAACCCATCCAGCAAGCAAAATAGAAGATACA  
 ACCAACCAAAACCAATCATTATCTTCCATCAGTAGCTGAAATTGAGATTCTGCT  
 CAGGCAGGAAGAGCATCTCCCAAAGTGCACACCCCTGTAACAGGGGGAAACATGGC  
 TACCTATGGCCATACCAACACATATAGTAGCTTACCAAGCCAGTACAGTCTT  
 GCAGCCAATAATCCAACAGAAAGTTATGGACCTCAGATACCTATTACAGGAGTC  
 GCAGACCTAGCAGTAGTGCACATCTCTCACACTACTGCAGACCCAGTCTCTCCA  
 GTCACCCCTCAGGTTCACACACCACTGCCTCGTCTTATTCACATTCTAGAAACAA  
 CAATACAGGTAACCTCCCTGTCCAGGCACCTGGGAAGAGAGAGGACAATTGGA  
 GCAGAGGGAGAGTAAAAACCCACATAGAACCCAGTTCTCCGACGGCATAGACAC  
 AGGACTGTGAGGCCAGCAATCAAGGGACCTGCTAACAAAAATGTGAGCCAAGTCC  
 AGCCACAGAGTACCCCTGGGATGTGCCACACATGTCCCTCCGAGAGGGCTCACAG  
 TGGCTACTGCAGCACTGTCAGTCCAAGTTCATCCCACAGTGCCTCCCCAAAAC  
 ATAATGTTGGGTCAAGCAGAACAGACTTACCAACTGTGGTCAAGAAACCAACTGTAC  
 TATTAAGGACAAACAAATGTAGATATTGAGATAATAACAACCAACTACAAATAT  
 TCCGGAGGGAAAGTAACCACGTGATTCTACGGAAGCAAGCATGACTCTGCTCC  
 AACATCTGTATCCCTGGGAAATCTCCTGTAGACAATAGTGGTCACCTGAGCATGCC  
 TGGGACCATCCAAACTGGGAAAGATTCAAGTGGAAACAACACCACCTCCAGCCCC  
 TCAGCACACCCCTCAATACCAACAAGCACAATCTCAAAGAGGAAAATCCCTTG  
 CACCAGATCTTGTAAATAACCAGAAGAAGAGGGATGTTAAAGAATCCATATCA  
 ATTGGTTACAAAAGAACCCAGCCGCAAAGCTCCAAAATAGCTCCTCTTAC  
 CACAGGTCAAGAGTCTCCCTCAGATTCTACAACTCTTGCACAAGTCCGCCACCAGC  
 TCTGTCTACAACAATGGCTGCCACTCAGAACAGGGACTGAAGTAGTATCAGGTG

CCAGAAGTCTCTCAGCAGGGAAAGAACGAGCCCCCACCAACTCCTCTCCAGTGCTTC  
CTAGCACCATAACGAAAGAGATCTAATACATTAAACTCTGTCAACGGAAACCCCCA  
CACTGACAAGTCCTACTGCTACTGCATCTGTCAATTATGTCTGAAACCCAACGAACAA  
GATCCAAAGAAGCAAAAGACCAAATAAAGGGCCTCGAAGAACAGAAACAAACAGC  
AAACACCACCCCCCAGGCAGGTTCTGGCTATACTGCATACTCAGCTCTAACAAACAGC  
TGATACCCCCCTGGCTTCAGTCATTCCCCACGACAAGATGATGGTGGAAATGTAAG  
TGCAGITGCTTATCACTCAACAACCTCTTCTGGCCATAACTGAACGTGTTGAGAA  
GTACACCCAGACTTTGGAAATAACACAGCTTGGAAACACAGTGTGAGCAAAT  
CACAGGAGAGTACCACTGAAAAGAGCCTCAGACACACCACCACTCCTCAGC  
AGTGGGGCGCCCCAGTGCCACTCCTCCCCACCTCCTTACTAAGGGTGTGGTT  
ACAGACAGCAAAGTCACATCAGCTTCCAGATGACGTCAAATAGAGTGGTCACCAT  
ATATGAATCTCAAGGCACAATAACAGATCTGCAGCAACCCCTCAGCAGAGGGTAGCC  
CCAATCCTGAGATCATAACTGGAACCAACTGACTCTCCCTCTAATCTGTTCCATCCAC  
TTCTGTGCCAGCACTAAGGGTAGATAAACACAGAATTCTAAATGGAAGCCCTCTCC  
CTGGCCAGAACACAAATACTCAGCTCAAGTCATACTCCGAAACCATTGAGAACGGCA  
AAAGGCCAGCAGTAAGCATGCCCCCACCTCAGCCTCCAGAGGCCAGCACTCAT  
GCCTCACACTGGAATACACAGAACGATGAGAAAGAGTGTGTTGATAAGAAC  
TGGTCAAACCCAACCTCCAAACATCTGCCCTACGTCTCTACCTAACAGACTCTATTG  
AAAAAGCCAAGAATAATTGGAGGAAAGGCTGCAAGCTTACAGTCCAGCTAAC  
AGACGTTTCTCCTGTGAGGCTGTGGAGACCCACTGCCCATCATCCACTGGACC  
AGAGTTTCACTCAGGANTGAAATATCCAAGGGACACAGAAAAGCCGTTCCACGT  
GCTTCCCCTGGCACCTGTCCATCCAGAGGGTCAGTATTCAAGGACCGTGGACAGTA  
CCTGTGCTCTGCATTAACTCCACTGGCGTAGACCATTTCATGTCCTTGTG  
GTTTTTACCCGGCAAGGATTGGAACAGACATGTCAAGGAGATCACAGITC  
GGAAGTACTGTGGAACAAAGTGCAGAGTGGAGGGTATGCCGAGGCCTACGGTTTC  
CTGGATACTTGCAAAACCAACGGTGGCTCAGAAACGGCAAGGAAGCAGAAAGG  
TCTGGTAACACCTGATGGAACATTGATCATCTATAATCTGAGTCTTATGATGTG  
GTTTTACAAGTGTGAGGCCAGCAACCCATCTGCCAGGATTCACTGTTGTTAAGA  
TACAAGTCATCACAGCTCCCCCTGTCAATTAGAGCAAAGAGGCAAGCCATGTTG  
GGGTTTACGGTGGAAAGTTGAAACTGCCCTGCACTGCAAAGGAACCTCCAGCTA  
GTGTTCACTGGGTCTTATGATGGGACTGAACCTAAACATTGCAAGTGTACTCATT  
CCAGATTCTCTGTATCCAATGGAACCTCTGTATATAAGAACATCGCTCCCTCAGT  
GAGGGCACTTATGAGTGCATTGCCACCAGCTCAGGCTCAGAGAGAACGGTAG  
TGATTCTACTGTGGAAGAGGGAGAGACAATCCCCAGGATAGAAACTGCCCTCTCAG  
AAATGGACTGAGGTGAATTGGGTGAGAAATTACTACTGAACGTGCTCAGCTACTGG  
GGATCCAAGCCTAGAATAATCTGGAGGCTGCCATCCAAGGCTGTCACTGACCAAGT  
GGCACAGAATGGCAGCCGAATCCACGTCTACCCAAATGGATCCTGGTGGTGGG  
TCAGTGACGGAAAAGACGCTGGTACTACTTATGTGTGGCAAGAACAAAATGGG  
AGATGACCTAGTCCTGATGCATGTCCGCCTGAGATTGACACCTGCCAAAATTGAACA  
GAAGCAGTATTAAAGAACAGTGCCTCATGGAAAGATTCCAAGTGTACTGCA

AGGCCTCTGGCTCCCTGTGCCTGAGGTATCCTGGAGTTGCCTGATGGGACAGTGC  
 TCAACAATGTAGCCCCAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCCT  
 TTCCACAATGGAACCTTGTATTCAACAACGTTGGGATGGCAGAGGAAGGGAGATTAT  
 ATCTGCTCTGCCAGAACACCTTAGGGAAAGATGAGATGAAAGTCCACCTAACAGT  
 TCTAACAGCCATCCCACGGATAAGGCAAAGCTACAAGACCACCATGAGGCTCAGGG  
 CTGGAGAAACAGCTGCCTTGACTGCGAGGTCACTGGGAACCGAAGCCAAATGTA  
 TTTGGTTGCTGCCTCCAACAATGTCATTCTCAATGACAGGTTCACATTTC  
 ATGCCAATAGAACCTTGTCCATCCATAAAGTGAAACCACCTGACTCTGGGACTATG  
 TGTGCGTAGCTCAGAATCCTAGTGGGATGACACTAACAGACATACAAACTGGACATT  
 GTCTCTAAACCTCCATTAAATCAATGGCCTGTATGCAAACAAAGACTGTTATTAAAGCC  
 ACAGCCATCGGCACTCCAAAAAAACTTGTACTGCAAGCAGATGGGATCCCATCT  
 TCCCAGGTACGTGGATTATGCCAGGCAATATTTCTCCAGCTCCATACTTTGGA  
 AGCAGAGTCACGGTCCATCCAAATGGAACCTGGAGATGAGGAACATCCGGCTTC  
 TGACTCTGCGGACTTCACCTGTGTGGTCGGAGCGAGGGAGGAGAGAGTGTGTTGGT  
 AGTGCAGTTAGAAGTCTAGAAATGCTGAGAACACCAACATTCAAGAAACCCATTCA  
 ACGAAAAAGTCATCGCCCAAGCTGGCAAGCCCTAGCACTGAACACTGCTCTGGAT  
 GGGAACCCCCCACCTGAAATTACCTGGATCTTACCTGACGGCACACAGTTGCTAAC  
 AGACCACACAATTCCCCGTATCTGATGGCAGGCAATGGCTCTCATCCTTACAAA  
 GCAACTCGAACAGTCAGGAAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCTA  
 CATCGAGAAACTCATCCTGTTAGAGATTGGCAGAACGCCAGTCATTGACATACGA  
 ACCAGGGATGGTGAAGAGCGTCAGTGGGAACCGTTATCACTGCATTGTGTC  
 ATGGGATCCCCAGCCAAATGTCAGTGGACTACACCGGGTGGCATGTAATCGAC  
 AGGCCTCAAGTGGATGGAAAATACATACTGCATGAAAATGGCACGCTGGTCA  
 AGCAACAAACAGTCACGCCAACAGAAATTATCTGTAAGGCTCAAAACAGTGTG  
 GCCAGGCAGTTATTAGCGTGTCACTGATGGTTGGCCTACCCCTCCCCGAATCATAA  
 ACTACCTACCCAGGAACATGCTCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGT  
 GTGGCCTGGGAATCCCCAAGCCAAAGTCACCTGGAGACGCCAACAGACTCCCT  
 GCTCTAAAAGCAACAGCAAGAAAACCCATAGAAGTGAAGATGCTTCACCCACAAG  
 GTACGCTGGTCATTCAAGATCTCCAAACCTCGGATTCCGGAGTCTATAAGTCAGAG  
 CTCAGAACCTACTTGGACTGATTACGCAACAACTTACATCCAGGTACTCTGACAGG  
 AAGGGGGAGACTAAAATTCAACAGAACGCTCACATCCACAGGGTTATTTTGGAA  
 GAAGTTAACAAAGGCAGCCATAGGCATGTAATGAGTCTGAATACATTACAGT  
 ATTAAATTACAATGGACATGCGATGAGACTTGTAAATGAAAGCATTGTGAACGTGA  
 AACCGAGTCTCTGTGGATCTCAAAGCAAACACTCTAACCTAAGGCACATTGATTG  
 CAACAAATAATAACAAACATTAAGAGAAAAAAATGATCCACTACGAAATAACAAAC  
 GGCTAATGCACCTGAATTCTCAGTAAAAGACCTTCTCGCTAACAGTTGCCAGC  
 TGCCTCGTGTCTGTTCTACCAATGTACAAACATCGCACACAGGGTGAATGGAGT  
 CAACGGGAAAGATTAAGTTGCAGGTCTGTGAAATCTCAATGTACAAATATTCTGTC  
 NCTGGTTATAAACATTGATAAAACGAAAAAAAAAAAAAAAAAAAAAAA  
 AAAA (SEQ ID NO: 1)

Figure 2

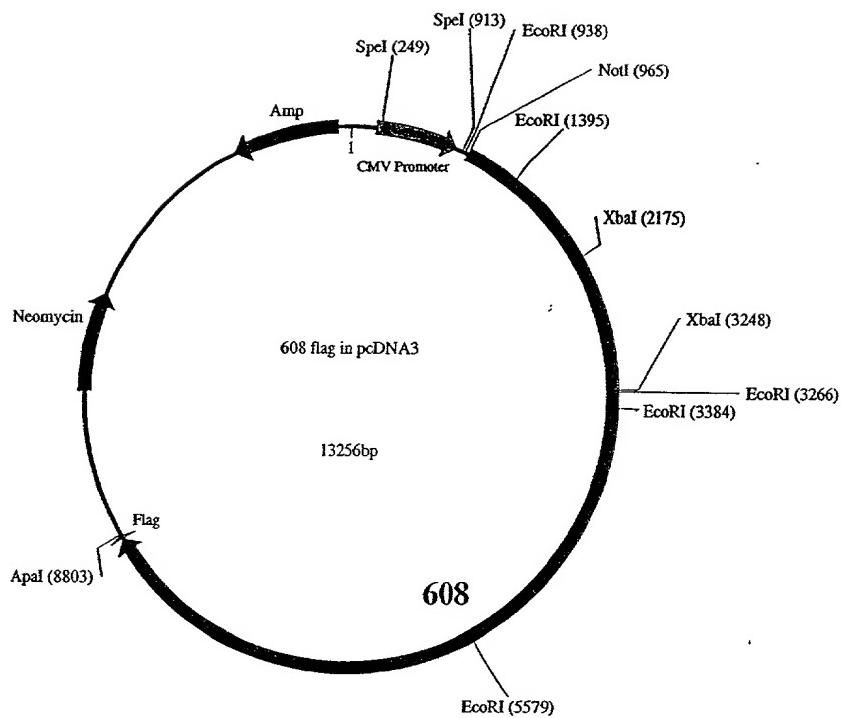


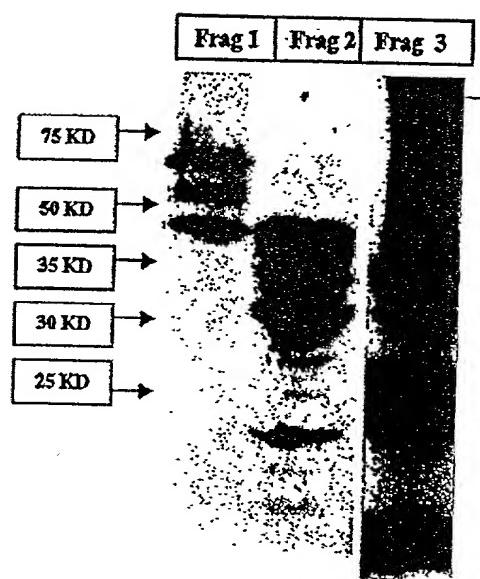
Figure 3

MQVRGREVSGLLISLTA VCLVVTPGSRACP RRCAC YVPTEVHCTFR YLTSIPDGIPANVE  
 RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGLQLVKMSYNKVQII  
 RKDTFYGLGSLVRLHLDHNNIEFINPEAFYGLTSRLVHLEGNRLLKHPDTFVSLSYLQI  
 FKTSFIKYLFSDNFTSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWMQGNPDI  
 IKCKKKDRSSSSPQQCPLCMNPRISKGRPFAMVPSGAFLCTKPTIDPSLKSLSVLTQEDNGS  
 ASTSPQDFIEPGFGLSLNMTXXSGNADMVCASI QKPSRTSPTAFTEENDYIMLNASFSTNL  
 VCSVVDYNIQPVWQLLALYSDSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEADVR  
 ADPFWFQQEKIVLQLNRTATLSTLQIQFSTDQAQIALPRAEMRAERLKWTMILMMNNPK  
 LERTVLVGGTIALSCPGKGDPSPHLEWLLADGSVKRAPYVSEDGRILIDKNGKLELQMA  
 DSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV  
 PDASISWILPGNTVFSQPSRDRQLNNGTIRLQVTPKDQGHYQCVAANPSGADFFFKV  
 SVQKKGQRMVEHDREAGGSGLGEPNSSVSLKQPASLCLSALTGSEAGKQVSGVHRK  
 NKHRDLIIRRGGDSTLRRFREHRRQLPLSARRIDPQRWAALLEKAKKNVPKKQENTTV  
 KPVPLAVPLVELTDEEKDASGMIPPDEFMVVLKTKASGVPGRSPTADSGPVNHGFMTSI  
 ASGTEVSTVNPQTLQSEHPDFKLF SVTNGTA VT KSMNPSIAS KIEDTTNQNPIIIFPSVAE  
 IRDSAQAGRASSQS AHPVTGGNMATYGHNTYSSFTSKASTV LQPINPTES YGPQIPIGV  
 SRPSSSDISSHTADPSFSSHPSGSHTTASSLFHIPRNNNTGNFPLSRHLGRERTIWSRG RV  
 KNPHRTPVLRRRHRRTVRPAIKGPANKNVSQV PATEYPMCHTCPSAEGLT VATAALS  
 VPSSSHSALPKTNNGVIAEESTTVVKKPLLFKDKQNV DIEIITTTKYS GGESNHVIPTE  
 ASMTSAPTS VSLGKSPVDSNGHLSMPGTIQTGKDSVETTPLPSPLSTPSIPTSTKESKRKTP  
 LHQIFVNNQKKEGMLKNPYQFGLQKNPAAKLPKIA PLLPTGQSSPSDSTLLTSPPPALST  
 TMAATQNKGTEVVSGARSL SAGKKQPFNTSSPVLPTISKRSN TLNFLSTETPTVTSPTAT  
 ASVIMSETQRTRSKEAKDQIKGPRKNRNNANTTPRQVSGY SAYS ALTTADTPLAFSHSP  
 RQDDGGNVSAVAYHSTSLLAITELFEK YTQTLGNTTA LETTLLSKS QESTTVKRA SDTP  
 PPLSSGAPPVPTSPPPPFTKGVVTD SKV TS AFQMTSNR VVTIYESSRHNTDLQ QPSAEAS  
 PNPEIITGTTDPSNLFPSVPA LRVDKPQNSWKPS PWPEHKYQLKSYSETIEKGKRP A  
 VSMSPHLSLPEASTHASHWNTQKHA EKS VFDKKPGQNP TS KHL PVYSLPKTLLKKP RIG  
 GKAASFTV PAN SDVFLPCEAVGDPLI IH WTRVSSGX EISQGTQ KSR FHVL PGNTL SI QRV  
 SIQDRGQYLC SAFNPLGV DHFHV SLSV FYPAR ILDRH VKEITV HFGST VELK CR VEG MP  
 RPTVSWILANQTVVSETAKGSRKVWVTPDGT LITYNLS LYDRGFYKCVASNPSGQD SLL  
 VKIQVITAPPVII EQKRQAIVGV LGGS LKLP CTA KGT P QPSVHWVLYDGT ELKPLQL THS  
 RFFLYPNTL YIRSIAPS VR GTYECIATSS SG SERRV VILTVEE GETIPRIETASQK WTEVN  
 LGEKLLLNC SATGDPKPRI WRLPSKAVIDQWHRM GS RJHV YPNGS LVVG SVTEK DAGD  
 YLCV ARNK MGDDLV LMH VRL RLTPAKIEQKQYF KKQV LH GKD FQV DCK ASG SPV PEV  
 SWSLPDGT VLN NVAQADD SGY RTK RY TLH NGT LYF NN VGM AE EG DYIC SAQ NTLG K  
 DEMKVHLTVLTAIPRIRQSYKTTMRL RAG ET A VL DCEV TGEPKPNV FWLLPSNNVISFS  
 NDRFTFHANRTLSIHVKPLDSDGYVCVAQNP SGDDT KTYKLDIVSKPPLINGLYANKT  
 VIKATAIRHSKKYFDCRADGIPSSQVTWIMP GNIFLPAPYFGSRVTVHPNGTLEM RNIRLS

DSADFTCVRSEGGESVLVVQLEVLEMLRRPTFRNPNEKVIAQAGKPVALNCSVGDGNP  
PPEITWILPDGTQFANRPHNSPYLMAGNGSLILYKATRNKSGKYRCAARNKVGYIEKLIL  
LEIGQKPVILTYEPGMVKVSGEPLSLHCVSDGIPKPNVKWTPGGHVIDRPQVDGKYIL  
HENGTIVIKATTAAHDQGNYICRAQNSVGQAVISVSVMVA YPPRIINYLPRNMLRRTGE  
AMQLHCVALGIPKPKVTWETPRHSLLSKATARKPHRSEMLHPQGTLVIQNLQTSDSGVY  
KCRAQNLGTDYATTYIQVL (SEQ ID NO: 2)

8/90

Figure 4



9/90  
Figure 5

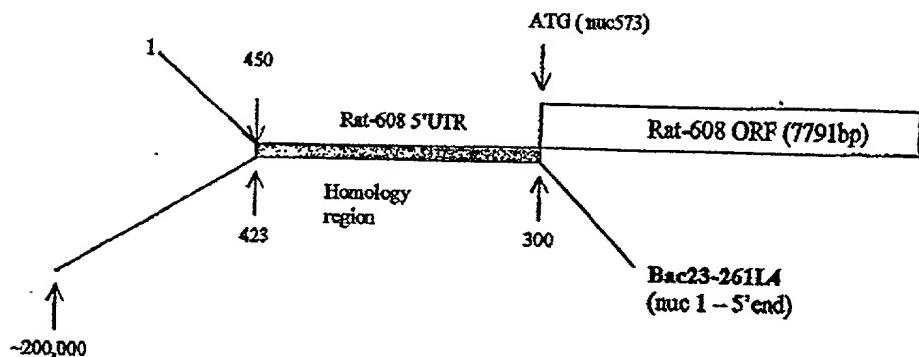


Figure 6

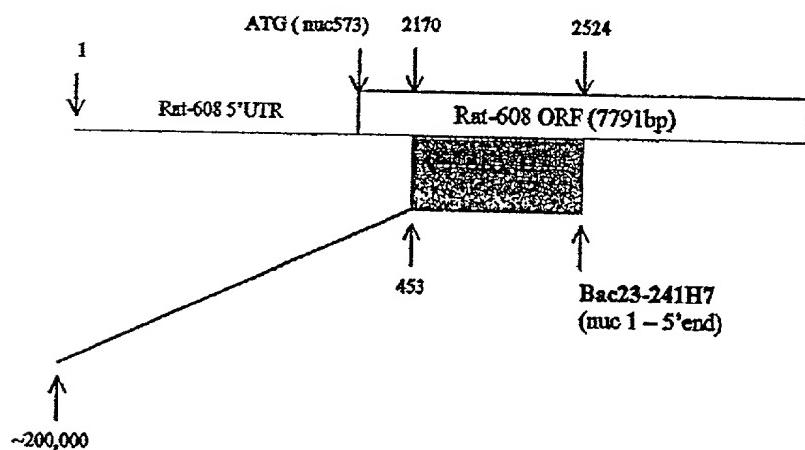


Figure 7

Nuc 1  
 ↓  
 TTTGGAACCAACCCAGATGCCCTAACAGAGAAATGGCCAGAAAATGGTGCATTAA  
 TCCAATGGAATACTACTCAACTTATTAAAACAACGACTTCATAAAATTTAGGCAAAT  
 GNAATGGTCTGNAGGATCTGAGTGGAGGTAACCCAAATCACAAGAACACTCATGGTATGC  
 ACTCACTGATAAGTGGCTATTGCTATGGTGTATTAAAAGGGAAAGAAGACACATAGC  
 TTTTGTTGTTATAATATTAAGATGAAATTGCCAGTGTGTGGCTATGAGTGAATCT  
 TGTTTCAGTGGATTACCGGAAGAAAATAATAAGTGAACTGTAGGAAGAAGTAGITAATCA  
 ↓ Nuc 390  
 AGGTGACAAAGTATGCCACATGGGAAAGACCCACAGTCCAGGAAACTGAGTCCTAA  
 GGATTCTATTAACCTCAGTCCCTCATGTCAGCTCTGAGACTTTGGCAGATCAGACACTT  
 AACCTCACCGCTCTACACAGCAGGCTACTATCCTCTGCACTTCACATGGAGTGTGA  
 CCATTAAGCTGCACTGAAACATGAGTGTACTGTTATAATCTTAAATACAAATTTGTT  
 TGTAAGTATGTAACCAAGACATGGTATGCTATTAAACCTTGTATGTTCTATGGACACT  
 TAATTTATGGTAGAAATGTCACAAAGCTTGTGGAGGCTGGAAAGATAACAAGGCTAAAGAG  
 GATGGCCTTTCAGTTTGAAGTAACTCAGTATGTTCTGGCATOCCCTTCTAAAGCA  
 ATTTAACCCCCCAAGTAGGCATAATTAAATGCTTACTTCATCAGAATATGCTAAATGAC  
 TCTCTAAACAGCTTGGTATAGGATCTAAATGTAATGTAATTAATGACATAAT  
 AAATAGGAGAAACCTGAGCTAGAATAGGTTAAATATGTCCTGGCTTCTAATAGGCTT  
 ATAGGTTATAAAAGGGGGAAAGGAATATTGAAACATCTAGAAGTAAATGATCCTG  
 AGTAGCGATCTGGGAAATACTGACTCTAACACACTGCAATCATCTCTGTGGTTTGC  
 GGAGCTGAGGTCTGGAAAGGCTCGACCTTGGTAAAGAATAACCTACCGAATACAGAGCTAT  
 GAOGTAGTGTGGAAAGGAGCTTGGAAAGAATGACAAGCTGAGTGTGCCCCAGAACATACTA  
 GATGCCATATTTCACAGGCAAGTGTGCACTGGGCAACTCTTAAAGATAAGGCTCTG  
 CAGTGTAAAGGACCTGTTGTCACACAGGCTCTCCAGGGTTAGTGTAACTCTGACTG  
 TTGACCTTAACTTACCTGATCATTAAATGACTAGAAATCACTTGGTGTAGCAACTG  
 GATATGGAATATTACTAATTGTAACCCAAAGCCTGGGCAACTCTAGCTTGGCAGCTCCATT  
 ATTCTGTTGGAGGCCAGTCACGGGGTTGTAACCTAACCTGACTCTTCTACTTACAAGACGC  
 ATTACCTGAGATGAGTCATTTCACAAAGCTTCTTAAAGAGCTAACTAGACATATTAGACATATT  
 CTGATGAGTAAAGCATATAAAAGTGGAGGAGCATGAAATGCTTCTCATGATGCTCATGGA  
 TGCTATTATAATGTTGAAATAAATGACTCTTAAAGGCTTATGATACTTGTCTACA  
 GAGTAAATCTCCATAAAATCATCTGCATTATAAAATTATTCTACATAATCCATCAATTAA  
 AAACCTTATGAAATTGTAACACAAAGATCCCCTAGGCCCTGGCCCTAGGATGGTGTGTA  
 TGGTGGCTGGAGAGATGGACCTAAAGACTTACTCTCCAGGAGCACATCTTCAGAAC  
 ATCTGCCCTAAACATTATGCCAAATGCTCATCAAAGGCTCACTCACATGTGCTTCACC  
 ACAGGGATTAAACAGTCATTGTCACATTCTCAACCCGCTGAGGCTGCTAGAGGAA  
 CAGGATGTTACGGATAACATCCAACCTTACAAAGGGATGTCATAACCTCACCACAA  
 AACAAACACGACAACAAACCCCTAAAAATTATCACGGCAATGAACTAAGGCAATGCA  
 GAAAAGTATTATGTCATGTTGGGTTTCTTCTTATAGTCAAATATGCAAGAAT  
 ATAGACAAAGATGGTTATGCAAGTGGGATGGCAAGGAGATACTGTGATTAGAGGAGCA  
 CAAGGCAACAAACTACAGAGTGAAGTAATCCAGAGACTTATGTTATATGAGGAGCTA  
 TTTAATAATTCTATTAAAGATAACAGCAAACGAGTGTATCTTACTAACACACACACTAC  
 ATAGAGAGATAAAGTGTAGATACTGTTGTTTATCTCATGTCAGTGTATAATTCTATAT  
 TGTCACCTCAACATGATAACCAACAAAGAGGGAAAGAGGCTAGGTGCTCTGCCAGGGC  
 GGAAGAGTACATTGCAAGGAGCTGAGACCCATTGTTAGGTGTCACCACTGGAGGGAGCTAGA  
 GAAAGTACGCCAAGGAGCTAAAGGGATCTGCAACCCCTATAGGTGGAAACAACATTATGAGCT  
 AACCACTACCCCGGGAGCTCTGACTCTAGTCATATATACAAAAGATGGCTAAATGG  
 CCATCACTGGAAAGAGGGGCCATTGGACTTGCACAAACTTATATGCCCCAGTACAGGGGA  
 ATACCCAGGGCCAAAAGGGGGAGTGGGTGGGCAAGGGGAGTGGGGGGGGGATATGGG  
 GGACTTITGGTATAGCATGGAAATGTAATGAGTAAATACCTAATAAAATGGAAAA  
 ↑ Nuc 2817  
 AAAAAAAAAAAAAAAAAAGGAAGGTCAAGACACCTCACTTCACGTCTATCTCAACTT  
 GCAAAACAGAAGGGGAGTCACAAACCCAGGACAAACACACAGTGTGAAAGGCTCTTGA  
 TGTTATTGCTGTTGTTGTTACCCACATCATTAGCATATATTCATTGAAACACTACGGGGT  
 CTATGACATGTTTCTTATCAAGTATATCACATGTCAGCATACTGGCACCACCTACCA

→ Nuc 3114

▼ Exam 1 (Nuc 3661)

GCTGGGGTTCAGGGCAGACAGAGGGTGGGATGGGAGAAGGGTGCAGGAAAAGGAAAGT  
ACTGGAGGGGAGTTGGACAAAAGCAGCGCCAAGGGAACATCGCTTCAGTACTGAAGCCA  
GGCAAAAGGAGGGAAAGGATTATAATGTAGCCTGGGAOGCTTCTATAAACACTGATGAGCTGT  
TGTGCAAAAGCAGCAATTGGAGGAAAAGCCGGGACGTCGGAAAGGAGGAGTATGCGATT  
ACTAGTGTAACTTGTAGGTAGTTGAGAACAATACTAACCTATATTGAGGAGAAGGAG  
AGCATTCCAGCAGCAGCAGCAGCAATCAGATAAAGGAAACCTTGGTTAGTTGGAA  
ATGTATGATAACCATTAAATAACAGAAGOGCTOCAGITCTCTGAAGAGTCAGTCCCCAGCTA  
TGAAAGACTAACGCCACTAACAGGCTTGTCTCCGGTGGAAAGCAAAGAAOGTCTTCCTAACATCAGG  
TGAAGGCTCTOCTCAGAGGATTTCTCTGCTCTGCTATGTTACAAGAGGATTCAAAAGCAAGAC  
AGAAGAGCTCAGTTAGTGCACATTCTT

REGISTRATION NO. 4 Dec 12/03

TGTTAAATACAGTGTAGGGCTTAAGTGTACGGGAACCTCATGGGTATTCACTTACGGCTCT  
CTCTCTATAACTAACTCTTAAGGGCATATAGTCCTCTCTGTTCCAGCTACCTCTGAC  
CATCTTGTATCTAATAATAGCAAGCTCATGCTTTAATCACTACGAGAGAGTATT  
CAAAAATATTCACTAGTGATGAAACAGTGACAGTGAGGCATAGAAGTAATCATTAGTAAATC  
TTAATTTGGTTAACCTCATAAACAGCTCCAGGGTGGGAGGGATCACAGGCCCTCGC  
CACGTGOGGGTTAAAGATTTCTAACAGAGAACGAGATCTCTCTGGCCATGCTCC  
CCATCACTGTCAGTAAAGCAGAGGGGTTTCCACAGCAGAGAACGAGACAGTGTTA  
TGCCCTGCAAAGTCAGCAGAGACTCAGGCCCTCCAGCTGGTCAGTTACTGCTCCGGTCAT  
AGTGGCTCTGAAAAGGOCATGTGCTTATIGCAGGACTTGAGACATGCTAGAAA  
GAAATTGACCTTTCTAGTGGTTATTACAGCTGAAAAGTATTGGAAGGTTAAAG  
CCAAAATAAATAAAACACATTTAAATAACAAATGTTACAAAATTGATCATATAAGA  
GTACATTCTATAATGCAATGTGAAAATATATAATTCTTATCTTACTGGTGCIAAG  
TTCTCAATGCACTGATCTACTTTTATTTTATTTAAATAAAATTATTTAAATGATATAAA  
AGTGTAAAAGGCTCTGGTCAAAACAAGAGAGTTAAATTACAAACTTAAATGICCCGAT  
AACATTATTATGCTTAATGACAGGGATCTGTTTCTGGAAATGAGAAGCTATG  
AAGATATGTTACAAATAAAGGCCATTAGTGTAAAGTCCATGGGAAGCTAGCACAC  
ACTGGTTTAAAGAGAACGACTTCCTGACTGCTAACGAGTTTACACTCTAGGGAAATAAG  
AGTGTCTCTCTCAGATTCACTAGCTTGTGTCATCATTTACTCTCTGATGATGAG  
CATTATAAGTGAATAAAGTAGGATCTAAAGGAATGCTAATTGGATGCCCTGAAACAA  
CTTCAAGGTTCTCTCTAGTCACTAGCTATTCAATTATGGATAATTGGGGATGGTGT  
TAATTTTTCTGAGTTCTATGGAATTCCAALAAACAAAAACAAACAAACAAACAAAAA  
ACCTCTGAAACTAGAACCTAACATCCTTACGCTGGTATGTAACAAAGAGAAATCTGCAC  
GAATTATGCTACATTGTTCTATTCAAGGACAGCCAAAGAATGTGGAAACCAACTTACGTA  
GCCGTCAAATATGAAAGGTTAAAGAAAATGTTGAAATGTCACAAAGAGATGCCCTG  
GCCATAAAAGGTGAAATCTGACATATGCAAGGAAATGGATGCACTGGAAATCAATTG  
GCCATAATCAAAACAAGACAGACTCAAAGGAAACACCGTGTTAGCTCTCTGACAAAC  
GAAGCTAGATTACCTGTAAGTGCCATGTTGTTAGAATTATTAGITATACACT  
ATTCTAATCTGAGTGTTGATAAAGGATGCACTGTAAGCAAAACAAAGCTAGTGGGG  
TOGGTAGGAGAGAAAGCAATGAGAGGAGTTAAATAGAACGAGCATAGTAACATAGGG  
CCAGGATGAAATGCTTAATTGCTTAACAAACCAAGACAGGAGGACACCGTCA  
AACCAGGGTGAATTCGCAAGCAGAGAACGGGAGAGTACACAAACAAATTGCGCAACTAA  
CAAGAACGGCTTCTGAGTGTGCTCTGCTGGGAGGGGCGTTCTCAGTTCTCTGAGCTGAC  
ACTGTTATAACAAACGTTGACAATACAAAGTGGCATGATGGATGTTTGTGCTATT  
TTCTAATTCTCTACTGTTGTTGTOGTGTTGTTGTTGTTGTTGCTGTGTTTCT  
ATTGTTCTCTTGTAGGAGAGGAGAACATGAAATTGGGTGTTGTTAGGAAGCTGAAACG  
&TCGGAAGAAGTGGGAAAGAGAAAATGTTGAGGACATATTAAACAAACAAACAA  
ACAAACAAAAGGTCTATTGCGCAACAAAGGGTGTGAAATTAAATTAACCGATGAC  
CTTAAAGAAAATATCCTAACATTCTCCAGAGTGTGCTATGTAATGCTGTCCTAGGACTT

### ▼ Exam 2 (Nuc 6559)

CTTGAACCTGGCCCTATAACCTCTGGTGCGGCTCTTCAGGATGCAGAACAGAGAGGCAGGGAA  
GTCACTGCTGTTGCTGATCTCCCTCACTGOCATCTGCGCTGGTGCACACCCCTGGAGGCAAGGGTC  
TGTCTCTGGCGATGTCCTGCTCATGTCGCCAACAGGGTGCACTGCTATTCTTGGGACCTGACCC  
TCCATCCTGGCAGGGCGATCCCAAGGCAATGTCAGGAAAGCTGCAATTAGGGTGTTGTT

Nuc 6755

GGACCTTGTGCTGATCTCCCTTCAGAGAGGGACCACRGATTTCCTCGTGACTCTTGCCCC  
AAACACCTGTGATTACTTTAATAGTTTCTCTAAAATGGGTCACTACAAACCTTATATIG  
TGGAGACAATGAACATTTATCCCAATAGTCTTACTAGAACCTGAAAGGCCCTCTTAGTT  
GTTGGGAGCCTCATATAATTGGGGCAGCTTATCTGAATGAAATTAAATGAAAGAGAT  
ACAGTTCTGTTAACATCATTATGATACCAAGGAQAGGAATTGTCTATTGATATTAA  
AAAGCATTCTTGCATTTATAAAACCCATTACAAAATGGCTACTTAAATACCTG  
CTTACTAAATCTGACAATTATGGTGATATTGAGGTITATGAAAATTGTTATGT  
ATAAATGCAACAAGAAATTGGGATATGCGCATCACCTATGTGCCATTAGTGAGGATGTACAGT  
ATGCGAACAAACTATTGTCAGCTTGGAGGAAGTAATGGGGGTTGGGGGCAACAAGGGT  
TATAACCGTATACCCAGTGGCTTGGAAAGCGATTCGAACACAGTAAGACTGACATTTGTT  
CTCCCTATGAGGGAGGGCCTTGGCTGAGCACTTGTCAATGAGCATTGCTCATTTGCT  
GGCAGGTTTATGATAACTTGACCCAAAGCTAGAGTCACTGGAGAGGAAGGAACCTCAACT  
GAGAACATGCGTGAAGAAGATCAGATTATAGGCAGGCCCTGTTGGGCAATTCTTAATTAG  
TGATTCTGGGAGGGCCAGTCATTGTCGGTACCTTCTCAGGCCACTTAAAAA  
AAAAAAAACAGGTGAGCAAGTCAGTCAAGGAGCAAGTCAGTCAAGCAGCAGGCCCTAATGA  
TCCTGTCATCAGCTCTGCCCAGTCAGTCCTACCCATTGAGTTCTGCTCTAGCTCCCTA  
CAGTGATGAAACAATGATGTGGAAAGTATAAGCCAAATAATCCTTCTCTCCOCAAACCTGCTG  
TTGGTCATGATGTTCTACAGTGATAATAGTCCTCATGAAGATCTGGTTATAACCA  
CTTGGTGGACTAAATCTGTATCTATAGCTGAGGAAAATGGAGCATGAAAGACTCCTCCAGA  
CTACACCAAGAGTGAAATCTGGGCTGAGCTTGAAGATCACACCCACAGTCAGTCACCTGCC  
GGGGCTTCTAAACGGAACACAGTTGAAAAGGGAAATTCTGTTGTTCTACATTGACA

## **Exon 3 (Nuc 8089) ↓**

TGTTGGACTTAAITGACGATTCATCTGAAGCTGAAAATGATTTCCTTCCAGGTATAACAGC  
CTCACTGAGCAGAACATGACTTCTGGCTCTGACCAGACTGGAGTTACTCTATGCTGCACA  
GCAATGGCATTCACAGACTCTGACAAAGCTCTTCGGCTCTGAGCTCTTGAGCAG

Nac 8218 4

GTGAGATAGGTAGAGGGTATGGAGGCAGAGAAGAGAGGGTGCACACTGTGGGTATAACCC  
AAAAGCTGCTGATTCCCGGGAGACATTCTATAAGCATTCTATAAACTAGAGGCAGATA  
TCAAGGAAGGATTTCATAATGCAATTCTATGAGAAAATTGAAATTAAAGGAAATATG  
CTGGGAAAATGCTAACCAAATGCGAGGACCTAATTGGATCTOCATAAGGCCACATAA  
AAAGCACAGCATGGGGCAGACACCCTGCAATTCCTGTCCCTGGAAGGCACCTGTCAGAA  
CCAGAGACTCATTGGCAAAACACTCTATTCAATGAAAGTCCATATTCAAGTGACAAA  
ACTTGACTCAGAAAACTAATGTTGGAAGGCATCAGGAAGCAGGCCAACCTGCTCTACT  
CATGCATGAATAAGGGATCCCGAGAGGAAGGGAAAGGAAAGGAAGGAAAGGAAAGG  
AAGGAAGGAGGAGGAAGGAGGAAGGAGGAAGGAGGAGGAGGAGGAGGAGGAGG  
AAGGAAGGAAAGGGAAAGGAAGGAGATGGGAGGGAGGGAGGAAGGAAGGAAAGG  
GGAGAAAGAGAGAAGGAAGGAAATAAAATAAATTTCAGGGATTATTACACCTTAA  
TTTATCCATAAAAGGTCTATTCCACCTGTTGCTGGAGTAGGTGGGATCCCTTATAT  
AAGGGCAGCTCTTAAACATAGTAGCATTTATAAACCATTACAAATTGAGTTCTCTC  
TTTATCCTCTACCATCTTCAAACTGAAACTACAAATTATCCCAAACTGAGAAGAAAATGC  
TGTAAAGAGTTTACACACAOOGAAGTGGGAAACTTAAAGGATTAGACAAGTCTAACATGAG  
AAATGGGAGAACAAAAGAGACTGCACAGGGAGCOCCTTCTCTCTTATAATCTGACAC  
TTGAGAAGCTAACTGACCTCTGCATGACTACTCACTCTTAAAGCAAAACATGCTGTGTT  
ATGAAAAGCACAATAAAAGTACATATGTCCTCATAATTCTCATCCTAAATTGAGCTGAGC  
AAATAATGCAATCAAGCAATAAACCCACTGTTCAAGAGACTTTAAACATGAAACTGGA  
ACTATGTCAGTTTGACTTAGGAGTACATAGTATGCTGTCCTGTATGTCACCAATGTT  
ATTAGGTCTACAGACAGCATTTGAAACATGTTCTCAGGGAGGAATCATCTATGCT  
GCATGAAAATCTCCACCTATGTTATCTCTTACAGCCAGGTTTCTCTGATGGAGAACATT  
GGGGTTGGGTTTACTCCAGGTAACATTAGGGAAAAGCTCTATGTTCTCAGTTGG  
CTTITATTTATGAGGGATGTTGTTATTCAGGAAAATTCTCTTGAAGAGATTACAAATT  
GGTCAAAACAGAAAATATGTAAGGTTATTGTTTATTAGTATTCATGTCCTTCT  
TTTAAATGGTATGCTAGAACTAATTAGATTAGATTAGATTAGAAAATAATC  
AGAGAGGGATTGATGAAATGCTAAAGCATTGCAAGGAAATTCTCAAAATTGCTCTAAT  
CAGAATCAATAATTCTATTAATTCTAAATTAGCAGCAOGCCAGATGTCGCGCAGCTGAG  
GAGTGGIAAAACTGTCAGCTGAGTGTCTATGAGTAAAGAGAGGAGTGAAGGGTTGAG

TGTGCGCTGCAACATCTGAAAACATTGGCTACATGATGGAAGCCAGGCACAAAAAGCC  
 ACATATIGCATGGGTTATGTTTATGAAATGTTAAAATACATGGATTCCTAGCAAACAGA  
 GTAAGATGTTACTTAGGGTCAGGAAAAGATTAAAAAAACTATTGATGTTGAAATG  
 ATCTTAATTGGGAAAAGACAATTCTAAGACGAAATGTTGAGGTAGATATAGTTAT  
 ATCCCTGTTGATATTGTAATAAACCAAGCATGCTGCTGCTGAGAAGGGCTAATGAAGGG  
 GCAGGAGGAAGTGAATGAGATGGTAGAAAGGAAGTCATATAOCATGGCTCTCTG  
 GGTGGAACTAGATATGTTAATATTGACATAAAGGAAGGAATGTTAGGGAAAGGATC  
 AAAACCAACAGGAGTGAGGGAGACATTAGGAACCAATGAGAGGGCAAAGTICATGGTCAA  
 TGTGTGAGACACCATATAAAACCTTCTTGTGCTAATCTAAACCACTAAACACTAAACAT  
 TAAAACAAAACATTTCGACAAGAATTATTATATTCAATAAAGATGTTAAATGGGG  
 GAAGTGAAGTICATTGATAGTCTCATATAATCTTAATGTTAATCTGCTTACGTT  
 TTATTATTAATTACTCTGCTGTCATTATTATCATCATTATCGTCATCATCATCACTA  
 ATGCTTTTACCCATACACAAATGTAAGGAGAGTGTAACTTCACTTAGTGAGGGAACTT  
 GGAGAGGGAAAGGGAGCGGATGCGGGGAGAGGCCACAGGAGGAGCTGAGAGGGAA  
 ATGAAACAAGAAAAAAATGTTGAGACATGCAACAAAATTCCATAGTCCACTACATTACTTG  
 TATTCTAATATTAAAGAAAATAATAAACCCATITCTGTGCACTTATCACCAGGCTAACAG  
 TTATCTGGCACAGATCTGCTCATGCACTTGTCCACCTGAGTCCACTTACGCTCTG  
 AATCCAATCCAGGGCATGCTTACTCTACACAGAACTAAAGATAAAGAGAGTTAA  
 AAGTAACCATGACATCTCTGTTCTTACTGCGATAAGTCTTAATATTATGGCTGCTTGT  
 GTATGTTCTAATTCTCTAATATTGTCACATITAGTGGCAACTACTTGTGTTGAATTGAGT  
 TGGAGTTAAGGTOCCATAGGATAATCTCAACATATTCTATATTAAACTTTCTCTCT

Exon 4 ? (Nuc 11286) ↓

TTGTGAAAGTTCCITTGAGAAAACAAATATGCCATATCTTCTTACAGGTCTAAAAATG  
 AGCTATAACAAAGTCCAAAATAATTGAGAAGGATACTTGTATGGACTCAGGAGCTTGAACCGG  
 TTGCAACCTGGATCACAAACATTGAGTTTATCAACCCGGGCTTACGGACTCACCTTGC  
 TOCGCTTGGTACATCTAGAAGGAAACCCGGCTGACAAGGCTCATCCAGACACATTGTCCTT  
 GAGCTATCTCCAGATATTAAAAACCTCTTCAATTAGNACCTGTACTTGTATGATAACTCATG  
 ACCTCCCCCTCCAAAAGAAATGGTCTCTATGCCAACCTAGAAAGCTTACTTGCAATGGAA  
 ACCCATGGACCTGTGACTGCAATTAAAGTGGTTGCOAGTGCAAGGGAAACCCAGGTA

Nuc 11680 ↑

ACTATCTTGTGTTGTTCTTCTTCTTATARKAGTATTCTCTCAATTCTTACATTAGAATGA  
 TATCCAAAAGTCCCCATAACCTCCCCCCCCACTTCTACCTACCCATTCCCTTCTTGG  
 CCTGGCATTCCTGACTGGGCATATAAAGTGTGCGGTTGCTTACGGACTCTCTTCTC  
 AGTGATGGCCAATAGGOCATCTTGTATACATATGCAAGCTAGGTCAAGAGCTCTGGGG  
 TACTGGTTAGTTCTATAATGTTGTTGCACTACAGGGTTGAA

Nuc 11967 ↑

(SEQ ID NO:3)

14/90

Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9

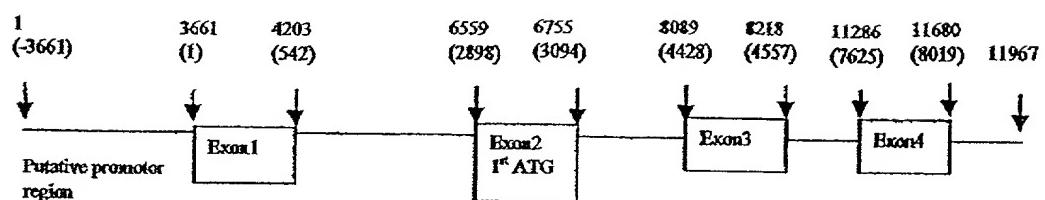


Figure 10

<i>cDNA_rat</i>	1	ogagagacgacagaaggtaacggctgcgagaagacgacagaagggtccag
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	51	aaaaaggaaagtgtcgggggagtggggacaaaagoagacgacaaagtga
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	101	atgcacttcaactgactgaggccaggcaaaacgogcggaggattttgt
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	151	gtagcttggaoaccttcataagacactgtatgacacgtttacgaaaaatag
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	201	aaattttagggaaaaacgcctgggccttoggaaagggtgtttagtagta
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	251	cttgcaagtttaggtactttaaggagaactaactaatgtatactattga
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	301	gggaggaggaagagcattacagatttccagcagcagcagggaaagcttg
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	351	gttaatttggaaaatggatgatagcattaaaataacagaagcgcctccagg
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	401	totctgaagcttcaagtccccagctgaaagccaaaaagactaagccac
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	451	taagcttttgtatccccttggaaagcaaactttccctccctgggtga
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	501	agactcttcgtcagaagatttcctgtctctgcctatgttacaagaggaatc
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	551	aaaaccaagacagaagagctcaggatgcaggtagggcaggaaagtca
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	601	cggttgttgcacccctactgtgtctgcgtggcaocccctggga
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	651	gcaggggctgtctcgccgtgtgcctgtatgtgcacagagggtgcac
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	701	tgtcacatttgcgttgcgtgcacccatccatccatggatcccgccatgt
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	751	ggaacgaataaaataggatataacagccctactatgtacagaaaaacg
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	801	actttgtatggcctgtggcaactggagttactcatgtgcacagtaatggc
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	851	attcacagagtcaactgacaagaccccttcggcgtgcagtcctgcaggt
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	901	ctaaaaatgagatataacaaagtccaaatcttoggaaaggataactttct
<i>genomic_hu</i>	1	-----

cDNA_rat	951	acggactcggagcttggccgggtcacctggatcacaacaacattgaa
genomic_hu	1	-----
cDNA_rat	1001	ttagcatcaaccctgaggcctttatggacttacctcgatccgttgtaca
genomic_hu	1	-----
cDNA_rat	1051	tttagaaggaaaccgyctcacaaagtcctccatccagacacatttgttcat
genomic_hu	1	-----
cDNA_rat	1101	taagctatctccagatatttaaaaacctctttcattaagtacctgttcttg
genomic_hu	1	-----
cDNA_rat	1151	tctgataacttcctgacctccctccaaaaagaatggtctctacatgcc
genomic_hu	1	-----
cDNA_rat	1201	aaacotagaaagectgtatTTGcatggaaacccatggacctgtgactgcc
genomic_hu	1	-----
cDNA_rat	1251	atTTAAAGTGGTTGtotgagtggatgoagggaaaccoagatataaaaa
genomic_hu	1	-----
cDNA_rat	1301	tgcaagaaaagacagaagotcttcoagtccctcagaaatgtcccccttgcatt
genomic_hu	1	-----
cDNA_rat	1351	gaacccccaggatctctaaaggcagaccctttgtatggtaaccatctggag
genomic_hu	1	-----
cDNA_rat	1401	ctttccatgtacaaagccaaaccattgtatccatcactgaagtoaaagago
genomic_hu	1	-----
cDNA_rat	1451	ctggttactcaggaggacaatggatctgcctccacctcacctaagattt
genomic_hu	1	-----
cDNA_rat	1501	catagaacccctttggctttgtttttgaacatgacananntntctggaa
genomic_hu	1	-----
cDNA_rat	1551	ataaggccgacatggctgttagtatccaaaaagccatcaaggacatccca
genomic_hu	1	-----
cDNA_rat	1601	actgcattcactgaagaaaatgactacatcatgotaaatgcgttcattttcc
genomic_hu	1	-----
cDNA_rat	1651	cacaatottgtgtcagtgttagattataatcacatccagccagtgtggc
genomic_hu	1	-----
cDNA_rat	1701	aacttctggctttatacagtgtactctcttotgtatactagaagaaagccc
genomic_hu	1	-----
cDNA_rat	1751	cagcttaccgagactccttcaactgtcttcttagatataaaaoagggtggtot
genomic_hu	1	-----
cDNA_rat	1801	taggctgaagacattttaccagcatagaggctgtgtcagagccagacc
genomic_hu	1	-----
cDNA_rat	1851	ctttttggttccaacaagaaaaattgttttgcagctgaacagaactgcc
genomic_hu	1	-----
cDNA_rat	1901	accacacttagoacattacagatocagtttccactgtatgtcaaatcgcc
genomic_hu	1	-----
cDNA_rat	1951	tttaccaaggcgagatgagagcggagagactcaaatggacoatgtatcc
genomic_hu	1	-----

<i>cDNA_rat</i>	2001	tgtatgtacaatccaaatggAACGACTGTACTGGTTGGCGGACT
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2051	attGCCCTGAGCTGTCAGGCAAAAGGGAACCCCTCACCTCAGTGGAAATG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2101	gtttotAGTGTGGAGTAAAGTGGAGAGCCCTTAAGTAGGGAGGATG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2151	ggcGAATCCATAAGACAAAAATGGGAGTTGAACTCAGATGGCTGAC
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2201	agctttGATGCAAGGTCTTACACTGCATAAGCACCAATGATGCAAGATGC
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2251	ggatGTTCTACACATAACAGGATAACTGTGGTAGAGCCCTATGGAGAAAAGCA
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2301	cacatGACAGTGGAGTCCAGCACACAGTGGTTACGGGTGAGACGCTGAC
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2351	cttccatgcctttccacGGGTGTTCCAGATGTTTATTAGTGGATTCT
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2401	tccAGGGAACACTGTGTTCTCTAGCCATCAAGAGACAGGCAAATTCTTA
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2451	acaatGGGACCTTAAAGAATATTACAGGTTACGCCAAAAGATOAAGGTCT
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2501	taccatGTTGGCTGCCACCOATCAGGGCCGACTTTCCAGTTAA
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2551	agtttcAGTTAAAAGAAAGGCCAAAGGATGGTGTGAGCATGACAGGGAGG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2601	caggTGGATCTGGACTTGGAGAACCCAACTCCAGTGTTCCCTTAAGCAG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2651	coAGCATCTTGAAACTCTCTGACATCAGCTTGAAGGGTCAGGGCTGG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2701	aaaACAAGTCTCCGGTGTACATAGGAAGAACAAACATAGAGACTTAAC
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2751	atCGGCGGCGTGGGATTCCACGCTCGGCGATTCAAGGGAGCATAGGAG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2801	cagTCCTCTCTCTGCTGGAGATTGACCGCAACGCTGGCAGCACT
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2851	tctAGAAAAGCCAAAAGAAATTCTGTGCAAAAAAGCAAGAAAATACCA
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2901	cagtaAAAGCCAGTGCCTGCTGGCTGTTCCCTCGTGGAACTCACTGACGAG
<i>genomic_hu</i>	1	-----
<i>cDNA_rat</i>	2951	gaaaAGGATGCCCTGGCATGATTCCCTCCAGATGAAGAAATTCTGTTCT
<i>genomic_hu</i>	1	-----

cDNA_rat_genomic_hu	3001	gaaaactaaggottctgggtc ooaggatccaaactgtctactotg 1
cDNA_rat_genomic_hu	3051	gaccagtaaatcatggtttatgaacgatatacgatcttcggcacaagaatgc 1
cDNA_rat_genomic_hu	3101	tcaactgtgaatocacaacactacaatctgagcaccttootgatttca 1
cDNA_rat_genomic_hu	3151	attatttagtgtaaacaacggtcagctgtgacaaadagtatgacccat 1
cDNA_rat_genomic_hu	3201	coatacgcaagaaaaatagaagatacaacccaaaaacccaaatcattatc 1
cDNA_rat_genomic_hu	3251	tttccatcagttagtctgaaattcggattctgtctgtcaggcaggaaagacatc 1
cDNA_rat_genomic_hu	3301	ttcocaaagtgcacacooctgtazacaggggaaacatggctacctatggc 1
cDNA_rat_genomic_hu	3351	ataccaacacatatagttagtgcattaccagcaaggccatcagttgcag 1
cDNA_rat_genomic_hu	3401	ccaataaaatccaaacagaaagttagtgcacccatcattacaggatc 1
cDNA_rat_genomic_hu	3451	cagcagacccatcagtagtgcacatcttctcaactactgoagacccta 1
cDNA_rat_genomic_hu	3501	gcttcctcaggtaacccttcagggtcacacaccactgcctgtttttt 1
cDNA_rat_genomic_hu	3551	cacattccatggaaacaaatacaggtaacttccoottgccaggcactt 1
cDNA_rat_genomic_hu	3601	gggaagagagaggacaatttggagcagagggagagttaaaaacccatata 1
cDNA_rat_genomic_hu	3651	gaaccccaggctccgcacggcatagacacaggactgtgaggccagoaatc 1
cDNA_rat_genomic_hu	3701	aagggacotgctaaacaaaatgtgagccaaagtccctccacagacttaccc 1
cDNA_rat_genomic_hu	3751	tgggatgtgccacacatgtcctccgcagagggtctcaagtggactgt 1
cDNA_rat_genomic_hu	3801	cagcactgtcagttccaagttcatccccacagtgccctccaaaaactaat 1
cDNA_rat_genomic_hu	3851	aatgttgggtcatagcagaagagtcttacactgttgtcaagaaaccact 1
cDNA_rat_genomic_hu	3901	gttactatthaaggacaaacaaaatgttagatattgagataataacaacca 1
cDNA_rat_genomic_hu	3951	ctacaaaatattccggggggaaagtaaccaogtgatctacggaaagca 1
cDNA_rat_genomic_hu	4001	agcatgacttctgtccaaacatgtatccctgggaaatctcctgtaga 1
cDNA_rat_genomic_hu	4051	caatagtgtccacctgagcatgcgtggaccatccaaactggaaagatt 1
cDNA_rat_genomic_hu	4101	cagtggaaacaaacaccacttcccagccccclcagcacaccctcaatacc 1

cDNA_rat	4151	acaaggcacaaaattctcaagaggaaactccottgcaccagatcttgt
genomic_hu	1	-----
cDNA_rat	4201	aaataaccagaagaaggaggggatgttaagaatccatatcaatttggtt
genomic_hu	1	-----
cDNA_rat	4251	tacaaaagaacccagccgcaaaagttccaaaatagtccttaccc
genomic_hu	1	-----
cDNA_rat	4301	acaggtcagagtccccctcagatttctacaactctttgacaaggccgoc
genomic_hu	1	-----
cDNA_rat	4351	accagctctgtctacaacaatggotgccactcagaacaaggccactgaag
genomic_hu	1	-----
cDNA_rat	4401	tagtatcaggtgccagaagtctctcagcagggaaagaagcagcccttcacc
genomic_hu	1	-----
cDNA_rat	4451	aactctctccactgtcttcctagcaccataagoaagagatctaatacatt
genomic_hu	1	-----
cDNA_rat	4501	aaacttcttgtaacggaaaccccacagtgacaagtctactgtactg
genomic_hu	1	-----
cDNA_rat	4551	catctgtcattatgtctgaaacccaaacgaaacaagatccaaagaagaaaa
genomic_hu	1	-----
cDNA_rat	4601	gaccaaataaaggggctcgaaagaacagaaacaacgcaaacaccacccc
genomic_hu	1	-----
cDNA_rat	4651	caggoaggtttctggctatagtgcataactcagetctaacaacagotgata
genomic_hu	1	-----
cDNA_rat	4701	cccccitggcttcagtcatccccacgacaagatgtatggtaatgtat
genomic_hu	1	-----
cDNA_rat	4751	agtgcagttgttatcactcaacaacotctttctgccataactgaact
genomic_hu	1	-----
cDNA_rat	4801	gttgagaagtacacccagactttggaaatacaacagctttggasacaa
genomic_hu	1	-----
cDNA_rat	4851	cgttgttagcaaatcscaggagagtaccacacgtgaaaagagcctcagac
genomic_hu	1	-----
cDNA_rat	4901	acaccaccaccactctcagcagtggggcgcccccagtgccactccttc
genomic_hu	1	-----
cDNA_rat	4951	cccacctctttactaagggtgtggttacagacagcaagtccatcatcag
genomic_hu	1	-----
cDNA_rat	5001	ctttccagatgacgtcaaataaggtggtcaccatataatgaatctcaagg
genomic_hu	1	-----
cDNA_rat	5051	cacaatacagatctgcagcaaccctcagcagaggctagccccatctga
genomic_hu	1	-----
cDNA_rat	5101	gatcataactgaaaccactgacttcccttaatctgtttccatccactt
genomic_hu	1	-----
cDNA_rat	5151	ctgtgccagcactaaggtagataaaccacagaattctaaatggaaagccc
genomic_hu	1	-----
cDNA_rat	5201	tctccctggccagaacacaaatatcagctcaagtctactccgaaaccat
genomic_hu	1	-----



cDNA_rat genomic_hu	6301 1	agaggaggagacaatcccccaggatagaaactgccttcagaaatggactg -----
cDNA_rat genomic_hu	6351 1	aggtaatttgggtgagaaattactactgaactgctcagctactgggat -----
cDNA_rat genomic_hu	6401 1	ccaaagectagaataatctggaggctgccatccaaggotgtcatogacca -----
cDNA_rat genomic_hu	6451 1	gtggcacagaaATGGGCAGCCGAATCCACGCTCACCAAATGGATCCTTGG -----TGGCAGCTGGATCCACGCTCACCTAATGGATCCCTGT
cDNA_rat genomic_hu	6501 40	tggttgggTCAGTGACGGAAAAAGACGCTGGTGA ttattggatCAGTAACAGAAAARGACAGTGGTGTCACTTGTGTGGCA
cDNA_rat genomic_hu	6551 90	AGAAACAAAATGGGAGATGACCTAGTCCTGATGCATGTccgcctgAGATT AGAAACAAAATGGGGAGATGATCTGATACTGATGCATGTTggctaAGACT
cDNA_rat genomic_hu	6601 140	GACACCTGCCAAAATTGAACAGAACAGTATTTAaAgAAGCAAGTGCCTCC GAAACCTGCCAAAATTGACCACAAAGCAGTATTTAaAgAAGCAAGTGCCTCC
cDNA_rat genomic_hu	6651 190	ATGGGAAAGATTTCAAGTGTGACTGCAaggcctctGGCTCCCCGTGCCT ATGGGAAAGATTTCAAGTAGATTGCAagttccGGCTCCCCAGTGCCA
cDNA_rat genomic_hu	6701 240	GAGGTATCCTGGAGTTGCCTGATGggacagtgcTCAACAATGTAGCCCA GAGATATCTGGAGTTGCCTGATGgaaaccatgtCAACAATGCAATGCA
cDNA_rat genomic_hu	6751 290	AGCTGATGACAGTGGCTATAGGACcaagaggtaACCCCTTTCCAAATG AGCCGATGACAGTGGCCACAGGACTtagggatataACCCCTTTCAACAATG
cDNA_rat genomic_hu	6801 340	GAACCTTGTATTCACAAACGTTGggatggcaGAGGAAGGGAGATTATATC GAACTTATACTTCAACAAAGTTGggtagcgGAGGAAGGGAGATTATACT
cDNA_rat genomic_hu	6851 390	TGCTCTGCCAGAACACCTTAAGGAAAGATGAGATGAAAGTCCACCTAAC TGCTATGCCAGAACACCTTAAGGAAAGATGAAATGAAGGTCCACTAAC
cDNA_rat genomic_hu	6901 440	AGTTCTAACAGCcattCCACGGATAAGGCAAAGCTACAAAGACCAACATGA AGTTATAACAGCtgtccccGGATAAGGCAAGATAACAAAACCAACAAGA
cDNA_rat genomic_hu	6951 490	GGCTCAggGCTGGAGAAACAGCTGTCCTTGACTGCGAGGTCACTGGGaa GAATCAaaGCTGGAGACACAGCTGTCCTTGACTGTGAGGTCACTGGGAt
cDNA_rat genomic_hu	7001 540	ccaaagccaaatgtATTTGGTTGCTGCCCTTCCAAatgtcATTTCATT cccaaaacaaaaaATTTGGTTGCTGCCCTTCCAAatgacatgtATTCCTT
cDNA_rat genomic_hu	7051 590	CTCCAATGACAGGTTCACATTCAAGCCAAAtgaaCTTGTCATCCATA CTCCATTGATAGGTACACATTCAAGCCAAAtgggtCTTGACCATCAACA
cDNA_rat genomic_hu	7101 640	AAGTGAAACCACTTGACTCTGGGGActatgtgtcgtagtcagAAATCCT AAGTGAAACTGCTCGATTCTGGAGAGtaactatgtgttagccccgaAAATCCC
cDNA_rat genomic_hu	7151 690	AGTGGGGATGACACTAACAGACATACAAACTGGAcattGTCTCTAAACCTCC AGTGGGGATGACACCAAAATGTACAAACTGGAtgtgGTCTCTAAACCTCC
cDNA_rat genomic_hu	7201 740	ATTAATCAATGCCCTGTATGCAAACAAagACTGTTATTAAGCCACAGCCa ATTAATCAATGGTCTGTATACAAACAGaaACTGTTATTAAGCCACAGCTg
cDNA_rat genomic_hu	7251 790	ttcgccacTCCAAAAAAATACTTGA tgagacatTCCAAAAAAACATTGACTGCAAGAGCTGAAGGGACACCAAtct
cDNA_rat genomic_hu	7301 840	tcccaaggtaatGTTGAGGCAATATTTCTCCAGCTCCATA cctgaagtcatGTGGATCATGCCAGACAAATTTCTCACAGCCCCATA

cDNA_rat	7351	CttTGGAAAGCAGAGTCACGGTCCATCCAAATGGAACCTTGGAgatgagga
genomic_hu	890	CtATGGAAGCAGAATCACAGTCATAAAAATGGAACCTTGGAAatttagga
cDNA_rat	7401	acatccGGCTTCTGACTCTGGCGACTTCACCTGTGTGGttcgagcgag
genomic_hu	940	atgtgaGGCTTCAAGATTCAGCCGACTTTATCTGTGTGGcccgaastgaa
cDNA_rat	7451	ggaGGAGAGAGTGTGTTGGTAGTGCAAGTTAGAAGTCTAGAAAATGCTGAG
genomic_hu	990	ggGGAGAGAGCGTGTGTTGGTAGTACAGTTAGAAGTACTGGAARTGCTGAG
cDNA_rat	7501	AAGACCAACATTCAAGAAACCCATTCAACGAAAagtcatcgcccaagctg
genomic_hu	1040	AAGACCGACATTAGAAATCCATTAAATGAAAAaatagtgtgccagctgg
cDNA_rat	7551	gcaaggcccgtagCACTGAJCTGCTGTGGATGGAAACCCCCCACCTGAA
genomic_hu	1090	gaaagtccacAGCATTGAATTGOTCTGTGATGGTAACCCACCACCTGAA
cDNA_rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTGCTAACAGACCAcacaa
genomic_hu	1140	ataatCTGGATTTACCAATGGCACACGATTTCCAATGGACCAcaaag
cDNA_rat	7651	ttccccGTATCTGATGGCAGGCATGGCTCTCATCCTTACAAAagcaa
genomic_hu	1190	ttatcaGTATCTGATAGCAAGCAATGGTCTTTATCATTTCTAAAacaa
cDNA_rat	7701	ctcggaacaagtCAGGGAACTATCGCTGTGCAGCCAGGAATAAGGTTGGC
genomic_hu	1240	ctcgggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAGGTTGGC
cDNA_rat	7751	TAcatcgagaaaactcatcctgttagagATTGGGCAGAACGCCAGTCATTCT
genomic_hu	1290	TAtatttgagaaaatttagtcataattagaaATTGGCCAGAACGCCAGTTATTCT
cDNA_rat	7801	GACATACGAACCAGGGAtggtaagagqcgTCAGTGGGAACCGTTATCAC
genomic_hu	1340	TACCTATGCACCAGGGAcagtaaaaggoTCAGTGGAGATCTCTATCAC
cDNA_rat	7851	TGCATTGTGTCTGATGGATCCCCAACGCCAATGTCAAGTGGACTACA
genomic_hu	1390	TGCATTGTGTCTGATGGATCCCCAACGCCAATATCAAATGGACTATG
cDNA_rat	7901	CCGGTGGccATGTAATCGACAGGCCCTCAAGTGGATGGAAAATACATAct
genomic_hu	1440	CCAAGTGGttATGTAGTAGACAGGCCCTCAAAATTAAATGGAAAATACATAtt
cDNA_rat	7951	GCATGAAAATGGCACGCTGGCATCAAAGCAACACAGCtcacgaccaAG
genomic_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAAGAAGCAACAGCttatgacagAG
cDNA_rat	8001	GAATTATATCTGTAGGGCTCAAAACAGTGTGGCCAggcagttattagc
genomic_hu	1540	GAAGACTATATCTGTAAGGCTCAAAATAGTGTGGTCAtacactgattact
cDNA_rat	8051	gtgtCAGTGTGGGTGTGGCTTACCCCTCCCCAATCATAAAActacctACC
genomic_hu	1590	gttcCAGTAATGTGTAGCCTTACCCCTCCCCAATTACAAAAtogtccACC
cDNA_rat	8101	CAGGAACATGTCAGGAGGACAGGGGAAGCCatgCAGCTCCACTGTGTGG
genomic_hu	1640	CAGGAGTATTGTCACCAGGACACGGGCAGCCTttCAGCTCCACTGTGTGG
cDNA_rat	8151	CCTTGGGAATCCCCAACGCCaaAAGTCACCTGGAGACGCCAAGACACTCC
genomic_hu	1690	CCTTGGAGTTCCCAAGCCAgAAATCACATGGGAGATGCCGTGACCACCTCC
cDNA_rat	8201	CTGCTCTCAAagcaacagcaagaasaccCATAGAAGTGGAGATGCTTCA
genomic_hu	1740	CTTCTCTCAcgccaaagttaaagagaggacacATGCCAGTGGAGCAGCTTCA
cDNA_rat	8251	CCCACAAGGTACGCTgGTCATTCAAGAATCTCAAACCTCGGATTCCGAG
genomic_hu	1790	CTTACAAGGTACCTaGTCATTCAAGAATCCCCAACCTCCGATTCTGGga
cDNA_rat	8301	tctTATAAGTGCAGAGCTCAGAACCTACTTGGactTGATTACGCAACAACT
genomic_hu	1840	taTACAAATGCACAGCAAAGAACCCACTTGGtagTGATTATGCAGCAACG
cDNA_rat	8351	TACATCCAGGTACTCTGACAGGAAGgggggagactaaaattcaacagaagt
genomic_hu	1890	TATATCAAGTAATCTGACATGAAatastaatgcaacaacatctgggca

cDNA_rat	8401	ccacatocacagggtTTTATTTGGAAAGAAGTTAACAAAGGCAGCCA
genomic_hu	1940	gaa-----TTTATTTGGAAAGAAGTTAACAAAGGCAGCCA
cDNA_rat	8451	TAGGCATGTAAATGAGtcTGAATACTTACAGTATTAAATTACAATGG
genomic_hu	1979	TAGGCATGTAAATGAAttTGAATACTTACAGTATTAAATTACAATGA
cDNA_rat	8501	ACATGCyatga-----GACTTGTAAATGAAAGCATTGTGAAC TGAAaccg
genomic_hu	2029	ACATGCaaaataaaagGACTTGTAAATAAATGCATTATGAAC TGAtgata
cDNA_rat	8546	agtctctg-----TGGATCTCAAAGCAAACTCTTAACCTAAGGCAC TTTg
genomic_hu	2079	otgatttatataatGGATCTCAAACAAACTTTAACCTAAGGCAC TTT
cDNA_rat	8591	ATTTGCCAACAAATAATAACAAACAttaagagaaaaaaatgatcCACTA
genomic_hu	2129	ATTTGCCAACAAATAACAATAAACAAacattgaaacggtt----CACTA
cDNA_rat	8641	CGAAAATAACAAACGGCTAATGCACCTGAATTctcagtaaaaagacottc
genomic_hu	2175	TAAAATAACAAATGGCTAATGTACCTGAATTttcagtaaaaaaaatgaac
cDNA_rat	8691	tctcgctaacagttgcCAGCTGCCTCGTGTGTTCCACCAATGT CAC
genomic_hu	2225	ttctataa-----CCAGTTGCCTAGTGTCCACCTCCTATCAATGT TAC
cDNA_rat	8741	AAACAtogcacacagggtGAATGGAGTCACGGGAAAGATTAAGTTGCG
genomic_hu	2268	AAGCAAtggcactca---GAACAGAGACAATGGAAAAATATTAATCTGCA
cDNA_rat	8791	GTctgtgtataatctca-----ATGTACAAATATTCTGtncTG
genomic_hu	2314	ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTG---TG

### exon1 (2342-2397)

cDNA_rat	8791	GTctgtgtaaatctca-----ATGTACAAATATTCTGtncTG
genomic_hu	2314	ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTG---TG
cDNA_rat	8829	GTTTATAAACATTTGATAAAACGGAAAAAAAAAAAAAAaaaaaaaaaaaaa
genomic_hu	2360	GTTTATAAACATTTGCTAACCTACAGAAAATAAGcactgaactgtc

(Genomic human OCP: SEQ ID NO:4)  
(cDNA rat: SEQ ID NO:5)

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~231 7	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

FIGURE 12

**608 Human translated nucleotide sequence (ORF)**

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTGGCTCCCTTGCTGT  
 GATCTGCCTGGTCGCCACCCCTGGGGCAAGGCCTGCCTGCCGCTGTG  
 CCTGTTATATGCCTACGGAGGTACACTGCACATTGGTACCTGACTTCCA  
 TCCCAGACAGCATCCGCCAATGTGGAACGCATCAATTAGGATACAAC  
 AGCTTGGTAGATTGATGGAAACAGATTTCTGGCCTGACCAAACAGGA  
 GITACTCATGCTCACAGCAATGGATTACACAAATCCCTGACAAGACCTT  
 CTCAGATTGCAGGCCTTGCGAGGCTTAAAAATGAGCTATAATAAGTCC  
 GAAAACCTCAGAAAGATACTTTTATGGCCTCAGGAGCTTGACACGATTG  
 CACATGGACACAAACAATATTGAGTTATAAAACCCAGAGGTTTTATGG  
 GCTCAACTTCTCCGCCGGTGCACTGGAAAGGAAATCAGCTCACTAACGCT  
 CCACCCAGATACATTGCTCTTGAGCTACCTCCAGATATTAAAATCTC  
 TTTCATTAAGTTCCTATACCTGCTGATAACTTCTGACCTCCCTCCCTCAA  
 GAGATGGTCTCCTATATGCTGACCTAGACAGCCTTACCTGCACTGGAAA  
 CCCATGGACCTGTGATTGCCATTAAAGTGGTTGTCTGACTGGATAACGCC  
 AGATGTAATAAAATGCAAAAAAGATAGAAGTCCCCTAGTGCTCAGCAGT  
 GTCCACTTGCATGAACCCCTAGGACTCTAAAGGCAAGGCCGTTAGCTATG  
 GTCTCAGCTGCACTTCCAGTGTGCCAAGCCAACCATTGACTCATCCCTG  
 AAATCAAAGAGCCTGACTATTCTGAAAGACAGTAGTTCTGCTTCATCTT  
 CCCCCAAGGTTCATGGCACCTTGGCTCCCTACTTGAATATGACAGAT  
 CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAGCCCTCAAG  
 GACATCACCATTGCATTCACTGAAGAAAATGACTACATCGTGTAAATA  
 CTTCATTTCAACATTTTGGTGTGCAACATAGATTACGGTCACATTCAAGC  
 CAGTGTGCAAATTGGCTTGTACAGTGATCTCCTGATACTAGAAA  
 GGAGCCACTTGTAGTGAACACCCGCACTCTATTACAAATATAAACAG  
 GTGGCTCTAACGCCTGAAGACATTACCAACATAGAGGCCAGATCTCAG  
 AGCAGATCCCTTGGTTAATGCAAGACAAATTCCCTGCAGCTGAACA  
 GAACTGCCACCACATTCACTGACATTACAGATCCAGTACTCCAGTGTGCT  
 CAAATCACTTACCAAGAGCAGAGATGAGGCCAGTGAACACACAAATGGA  
 CTATGATITCAAGGGATAACAATACTAAGCTGGAACATACTGTCTGGTA  
 GGTGGAACCGTTGGCTGAACTGCCCAGGCAAGGAGACCCCCACCCACA  
 CGTGGATTGGCTCTAGCTGATGGAAGTAAAGTGAGAGGCCCTATGTCA  
 GTGAGGATGGACGGATCTTAATAGACAAAAGTGGAAAATGGAACTCCA  
 GATGGCTGATAGTTTGACACAGCGTATATCACTGTATAAGCAGCAATT  
 ATGATGATGCAAGATATTCTCACCTATAGGATAACTGTGGTAGAACCTTGG  
 TCGAAGCCTATCAGGAAAATGGGATTCTACACAGTTCATTGGTGAA  
 AACCTGATCTCCATGCCATTCTACTGTTATCCAGATGCCCTATTAGC  
 TGGGTTATCCAGGAAAACATGTGCTCTACGTCATCAAGAGACAAGAA  
 AGTCTAAACAAATGGCACATTAAGAATATTACAGGTACCCCGAAAGACC  
 AAGGTTATTATCGCTGTGGCAGCCAACCCATCAGGGGTTGATTTTGAA  
 TTTCCAAGTTCACTGCAAGATGAAAGGACAAGGCCCTGGAGCATGAT  
 GGAGAAACAGAGGGATCTGGACTTGATGAGTCAATCCTATTGCTCATCT  
 TAAGGAGGCCACCGAGTGACAACTCCGTACATCTGCTGTGAGGCCGCTG  
 AGGTGGAAAACACACCTCAAGCACAAGTAAGAGGCCACAACATCGGGA  
 ATTAACACTCCAGCGACGTGGAGATTCAACACATCGACGTTTAGGGAGA  
 ATAGGAGGCATTCCCTCCCTGCTAGGAGAATTGACCCACAACATTGG  
 GCGGCACTGTTGGAGAAAGCTAAAAAGAATGCTATGCCAGACAAGCGAG  
 AAAATACCAAGTGAGGCCACCCCAAGTGGTACCCAACTCCCAACATA  
 CCTGGTGAAGAAGACGATTCCCTAGGCATGCTCGCTACATGAGGAATT

TATGGTCCCGGCCACTAAAGCTTGAACCTTCCAGCAAGGCAGTGACTG  
 CTGACTCCAGAACAAATATCTGATAGTCCTATGACAAACATAAATTATGGC  
 ACAGAATTCTCTCTGTGAATTCAAATACCAAGGCACCAATCAACATT  
 ACAGATTCAAACATGTCTACTGCTATTAAAATACAGCCATGTCAAAGAA  
 TATAAACCCAACCAGTCAAGCCAAATACAAGGCACCAATCAACATT  
 CATCCACTGTCTTCCACTGCTACTGGAGCAACTGAATTCAAGGACTCTG  
 ACCAGATGGGAAGAGGAAGAGAGCATITCCAAAGTAGACCCCCAATAAC  
 AGTAAGGACTATGATCAAAGATGTCATGTCAAATGCTTAGTAGCACCA  
 CCAACAAACTATTAGAGTCAGTAATACCACAAATAGTCATCACAGACA  
 TCTGTAAGAGAAGTGAAGTGAACCCAGGCACAACTCACTTCTATTCTCACAC  
 TACTCAAATACCTAGCACCTCCACGTTCCCTCAGATCCACACAGCTGC  
 TCATTCTCAGTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGT  
 CAGACGCTTGGAGGCAGAGGAAAATTGGCGAAGGGGGCGGATTATC  
 AGCCCCATATAGAACTCCAGTTCTGCAGCGCATAGATACAGCATTTTCAG  
 GTCAACAAACAGAGGTTCTCTGAAAAAAAGCACTACTGCATTCTCAGCCA  
 CAGTGCATGACATGTGACATGTCTGTCTGTCTCCAGGGAGAGGCTCACCA  
 CTGCCACAGCAGCATGTCATTCAGTGTCTGCTCCCACACCTTCCCA  
 AAGCTGACATGCTAGAGTCCCATCAGAAGAGTCTACAACACTCTAGTCCAG  
 AATCCCACTATTACTACTTGGAAACAAACCCAGTGTAGAGAAAACACACC  
 CACAATAAAATATTCAAGGACTGAAATTCCAAGTGACTCCAACGGTGTG  
 CAGTCATGACATATGCTCAACATCCATACCCATGGAAAAAAACTCACAAA  
 GTAAACGCCAGTACCCACGTGTCTAGCACCAATGAAGCTAAAGAGA  
 TTCACTGATTACATGTCACCTTCAGGTGCTATACCCAAGCCACCAATGAC  
 TATTATAGCCATTACAAGGTTCTGAAAGGAAAATTCCCTGGCAACAGA  
 ACTTTGTAATAACCATAACCCAAAGGCAGATTAGGAATCAACATAAA  
 GTTAGTTACAAAAAAGCACAGCTGTGATGCTTCTAAACATCTCTGCT  
 TTACCCACAGACAAAGTTCCCTTCCATTCAACACTTCAACAAAGT  
 GTGATGCAAAATCCATTAACCTTGACTACCGCTCACCAACTACGACC  
 AAAACACACAATCTGGAAGTCTCCAACAAAGAAGGAGCTTCCCTTCC  
 ACCCTTAACCCATGCTCTAGTATTATAAGCAAAGACTCAAGTACAA  
 AAAGCATCATATCAACGCAAACAGCAATACCAAGCAACAACCTCCTACCTC  
 CCTGCATCTGTCATCACTTATGAAACCCAAACAGAGAGATCTAGAGCACA  
 AACAAATACAAGAGAACAGGAGCCTCAAAAGAAGAACAGGACTGACCCA  
 AACATCTCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACA  
 CCTCTGCTCTGGCATTCACTCATCCCCACCAAGAAAACAACACTGGGATT  
 TCAAGCACAATCAGTTCTGATGAAAGACTCTTAATCTGACAGATGTGATT  
 GAAGAACTAGCCAAAGCAAGTACTCAGACTTGAAGAGGACAATTGCTTC  
 TGAAACAAACTTGTCCAGCAATCACCCAGAGTACCTGACTACCCACTGCTATGACA  
 CATCATTAGACACTCCCATACCCATTCTGAGCAGCAGTGTCTACTCTAA  
 TGCCAGTTCCCATCTCCCTCCCTTACTCAGAGAGCAGTTACTGACACAC  
 GTGGCGACTCCCATTCCGGCTTATGACAAATACAGTGGTCAAGCTGAC  
 GAATCCTCAAGGCACAATCTCCAAATGCCAGTTCAACATTGGAAACCACT  
 CACTTCATCTACCTCTAACTGTTACATTCTACTCCCATGCCAGCACTAAC  
 AACAGTTAAATCACAGAATTCCAATTAACCTCATCTCCCTGGCAGAAT  
 ACCAATTGGCACAAACCAACTCAGACATTGCTAAAAAGGCAAAAG  
 CCAGAAGTAAGCATGGTGGCTACTACAGGCCTGTCCGAGGCCACCACTCT  
 TGTTTCAGATTGGGATGGACAGAAGAACACAAAGAAGAGTGACTIONGATA  
 AGAAACCAGTCAAGAAGCAACAACTTCCAACCTCCCTCCCTTGACTCTT  
 TGTCTAGGTATATATTGAAAAGCCCAGGATAGTGGAGGAAAAGCTGCA  
 AGTTTACTATTCCAGCTAACTCAGATGCCCTTCTCCCTGTGAAGCTGTT

GGAAATCCCTGCCACCATTGACCAGAGTTCAAGACTTGATTA  
 TCTAGAGGAACCAAGAACATGCAGGGTCCAGGTCTCCCAATGGTACCC  
 GTCCATCCAGAGGTGAAATTCAAGGACCGCCGACAGTACTTGTGTTCCG  
 CATCCAATCTGTTGGCACAGACCACCTCATGTCACCTTGTCTGTT  
 CCTATCCTCCCAGGATCTGGAGAGACGTACCAAAGAGATCACAGTCAT  
 TCCGGAAGCACTGTGGAACGTGAGCAGAAGGTAGGCCAAGCC  
 CTACAGTTACCTGGATTCTGAAACCAAACAGTTGTCTCAGAATCATCCC  
 AGGGAAAGTAGGCAGGCTGTGGTACGGTACGGAACATTGGCTCCAC  
 AATCTCAGTATTIATGACCGTGGTTTACAAATGTGTGGCAGCAACCCA  
 GGTGGCCAGGATTCACTGCTGGTAAATAACAAGTCATTGAGCACCACC  
 TGTATTCTAGAGCAAAGGAGGCAAGTCATTGAGGACTTGGGTGAAA  
 GTTAAAACGCCCCGTACTGCAAAAGGAACCTCTCAGGCCAGCGTTACT  
 GGGTCTCTGATGCCACTGAAGTGAACCTACAGTTACCAATTCCA  
 AGTTGTTCTTATTCAATGGACTTGTATATAAGAAACCTAGCCTTT  
 CAGACAGGGCACTTATGAATGCATTGCTACCAGTCCACTGGTCGGAG  
 CGAAGAGTAGTAAATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGA  
 TAGAAGCTGCATCCCAGAAAAGGACTGAAGTGAATTGGGACAAATTA  
 CTACTGAACTGCTCAGCCACTGGGAGCCAAACCCAAATAATGTGGAG  
 GTTACCATCCAAGGCTGTGGTCGACCAGTGGAGCTGGATCACGTCTACC  
 CTAATGGATCCCTGTTATTGGATCAGTAACAGAAAAGACAGTGGTGTCTC  
 TACTTGTGTGGCAAGAAAACAAATGGGGATGATCTGATACTGATGCA  
 TGTAGCCTAAGACTGAAACCTGCCAAATTGACCAAGCAGTATT  
 GAAAGCAAGTGCCTCATGGGAAAGATTCCAAGTAGATTGCAAGCTTCC  
 GGCTCCCGAGTGCAGAGATATCTGGAGTTGCTGATGGAACCATGAT  
 CAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATAT  
 ACCCTTTCAACATGGAACCTTATACTTCAACAAAGTTGGGTAGCGGA  
 GGAAGGAGATTATACTGCTATGCCAGAACACCCCTAGGGAAAGATGAA  
 ATGAAGGTCCACTTAAAGTATAACAGCTGCTCCGGATAAGGCAGAG  
 TAACAAAACCAACAAGAGAATCAAAGCTGGAGACACAGCTGCTTGTACT  
 GTGAGGTCACTGGGATCCAAACCAAAATTITGGTGTGCTGCCCTTCC  
 AATGACATGATTCTCTCCATTGATAGGTACACATTCTGCAATGGG  
 TCTTGACCATCAACAAAGTGAACACTGCTGATTCTGGAGAGTACGTATG  
 TGTAGCCCAGTCCAGTGGGATGACACCAAAATGTACAAACTGGATG  
 TGGTCTCTAAACCTCATTAAATCAATGGTGTGTATACAAACAGAACTGTT  
 TTAAAGGCCACAGCTGTGAGACATTCCAAAAACACTTGTACTGCAGAGCT  
 GAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGACAATT  
 CCTCACAGCCCCATACTATGGAAGCAGAACATCACAGTCATAAAATGGAA  
 CCTTGGAAATTAGGAATGTGAGGCTTICAGATTGAGCCGACTTATCTGTG  
 TGGCCGAAATGAAGGTGGAGAGAGCGTGTGTAGTACAGTTAGAAGTA  
 CTGAAATGCTGAGAAGACCGACATTAGAAATCCATTAAATGAAAAAAT  
 AGTTGCCAGCTGGAAAGTCCACAGCATTGAATGCTCTGATGGTA  
 ACCCACCACCTGAAATAATCTGGATTACCAATGGCACACGATTCCA  
 ATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTCTTATCA  
 TTCTAAAACAACCTGGGAGGATGCGAGAAAATATCGCTGTGAGCTAGG  
 AATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATGGCCAGAA  
 GCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAGGCATCAGTGGAG  
 AATCTCTATCACTGCATTGTGTCTGATGGAATCCCTAACGCCAATATCA  
 AATGGACTATGCCAAGTGTGTTATGTAGTAGACAGGCCCTAACATTAAATGGG  
 AAATACATATTGCATGACAATGGCACCTAGTCATTAAGAAGCAACAGC  
 TTATGACAGAGGAAACTATATCTGTAAGGCTAAATAGTGTGGTCATA

CACTGATTACTGTCCAGTAATGATIGTAGCCTACCCCTCCCCGAATTACAA  
ATCGTCCACCCAGGAGTATTGTCAACCAGGACAGGGGCAGCTTCAGCTC  
CACTGTGTGGCCTTGGGAGTTCCAAGGCCAGAAATCACATGGGAGATGCC  
TGACCACTCCCTTCTCTAACGGCAAGTAAAGAGAGGACACATGGAAGTG  
AGCAGCTTCACTTACAAGGTACCCTAGTCATTAGAATCCCCAACCTCC  
GATTCTGGGATATAAAATGCACAGCAAAGAACCCACTTGGTAGTGATTA  
TGCAGCAACGTATATTCAAGTAATCTGA

29/90

Figure 13

**A**

Region			Region Length	% identity	% positives	% gaps
General	Rat	Human				
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
Total	Alignment		2614	62	74	1

**B**

Region			% identity	% positives	% gaps
Rat	Mouse	Length			
1-238	1-238	238	91	92	1

**C**

Region			Region Length	% identity
General	Rat	Human		
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
Total	Alignment		7842	80

**D**

Region			Region Length	% identity
General	Rat	Mouse		
1-720	1-718	1-720	720	93

Figure 14



rat_cdna human_5+3_corrected mus_cdna_5	AAGAAAATGACTACATCATGCTAAATGGTCATTTCACAAATCTTGTTGCAAGTGTAG AAGAAAATGACTACATCGTGCATAATCTCATTTCAACATTTGGTTGCAACATAG
rat_cdna human_5+3_corrected mus_cdna_5	ATTATAATCACATCCAGCCAGTGTGCCAACITCTGGCATTATACTGACTCTCTCTGA ATTACGGTCACATTCAGCAGTGTGGCAATTTCGGCTTGTACAGTGTATTCTCTCTGA
rat_cdna human_5+3_corrected mus_cdna_5	TACTAGAAAGGAAGCCCAGCTTACCGAGACTCCTTCACITGCTCTAGATATAAACAGG TACTAGAAAGGAGCCACTTGTCTTGTAAACACCGCAGCTCTTACAATATAAACAGG
rat_cdna human_5+3_corrected mus_cdna_5	TGGCTCTTAGGCTGAAGACATTTCACCACATAGAGGCTGATGTCAGAGCAGACCTT TGGCTCTTAAGGCTGAAGACATTTCACCACATAGAGGAGATCTCAGAGCAGATCCCT
rat_cdna human_5+3_corrected mus_cdna_5	TTTGGTTCCRACAAGAAAAATTGCTTGCAAGCTGAACAGAACTGCCACACCTAGCA CTTGGTTAACGAAAGACCAATTTCCTTGCAAGCTGAACAGAACTGCCACACATTAGTA
rat_cdna human_5+3_corrected mus_cdna_5	CATTACAGATCCAGTTTCCACTGATGCTCAAATCGCTTACCRAGGGCGGAGATGAGAG CATTACAGATCCAGTACTCCAGTGTGCTCAAATCTTACCAAGAGCAGAGATGAGGC
rat_cdna human_5+3_corrected mus_cdna_5	CGGAGAGACTCAAATGGACCATGATCCTGATGATGAAACATGCCAACTGGAAAGCACTG CAGTGAACACAAATGGACTATGATTCAAGGGATAACATACTAGCTGGAAACATACTG
rat_cdna human_5+3_corrected mus_cdna_5	TCCTGGTTGGCGGCACTATTGCCCTGAGCTGTCCAGGCAGGCCCTTCACCTCACT TCTGGTTAGGTGGAACCGTTGGCTGAACTGCCAGGCAGGAGACCCCCACCCACACG
rat_cdna human_5+3_corrected mus_cdna_5	TGGAATGGCTCTAGCTGATGGAGTAAAGTGAGAGGCCCTTACGTTAGCGAGGATGGGC TGGATTGGCTCTAGCTGATGGAGTAAAGTGAGAGGCCCTTATGTCAGTGAGGATGGAC
rat_cdna human_5+3_corrected mus_cdna_5	GAATCCTTAATAGACA AAAATTGGGAAGTTGGAACCTGCAGATGGCTGRCAGCTTTGATGCGAG GGATCTTAATAGACA AAAAGTGGRAAAATTGGAACTCCAGATGGCTGATAGTTTGACACAG
rat_cdna human_5+3_corrected mus_cdna_5	GCTTTACRCTGCATAAGCAGCAATGATGCAAGATGGGAAGTGTACATACAGGATAA GGCTATATCATGTATAAGCAGCAATTATGATGATGCAAGATATTCTACCTATAGGATAA
rat_cdna human_5+3_corrected mus_cdna_5	CTGTGGTAGGGCTATGGAGAAAGCACACATGACAGTGGAGTCAGCACACAGTGGTTA CTGTGGTAGAACCTTGTGCGAACCTATGGAAATGGGATTCATCACACAGTTTCA
rat_cdna human_5+3_corrected mus_cdna_5	CGGGTGAGAGCCTCGACCTTOCATGCTTTCCACGGGTGTCCAGRTGCCTCTATTAGCT TTGGTGAAACACTGTGATCTCCATGOCATCTACTGGTATCCAGATGCTCTATTAGCT
rat_cdna human_5+3_corrected mus_cdna_5	GGATTCTCCAGGGAAACACTGTGTTCTCTAGCCATCAAGAGACAGGCAAATTCTAAACA GGGTTATTCCAGGAAACATGTGCTCATCAGTCATCAAGAGACAGGAAAGTTCTAAACA

rat_cDNA human_5+3_corrected mus_cDNA_5	ATGGGACCTTAAGAATATTACAGTTAOGCCAAAAGATCAAGGTCAATTACCAATGTGTCG ATGGCACATTAAAGAATATTACAGTCACCCCGAAAGACCAAGGTATTATCGCTGTGTCG
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGCCAACCCATCAGGGGCCGACTTTTCCAGTTAAAGTTCAAGTCAAAAGAAAGGCC CAGCCAACCCATCAGGGTTGATTTTGATTTCAAGTCAAGATGAAGGAC
rat_cDNA human_5+3_corrected mus_cDNA_5	AAAGGATGGTTGAGCATGACAGGGAGGCAGGTGCACTGGACTTGGAGAACCCAACTCCA AAAGGCCCTGGAGCATGATGGAGAAACAGAGGGATCTGGACTTGATGAGTCATAATCCCA
rat_cDNA human_5+3_corrected mus_cDNA_5	GTGTTTCCCITAAGCAGCCAGCATCTTGAAGAACTCTCTGCATCAGCTTGAACAGGGTCAG TTCATCTAAGGAGCCACCAGGTGCAACAACCTCGTACATCTGCTCTGAAGGAGGCTG
rat_cDNA human_5+3_corrected mus_cDNA_5	AGGCTGGAAAACAACTGTOCCGGTGTACATAGGAAGAACATAGAGACTTAATACATC AGGTTGGAAAACACACCTCAAGCACAAGTAAGGGCACAACATACGGGAATTAAACACTCC
rat_cDNA human_5+3_corrected mus_cDNA_5	GCGGGCGTGGGGAATTCCACCGCTCOGGCGATTCTGGGAGCATAGGAGGCAGCTCCCTCT AGCGAGGTGGAGATTCAACACATCTGGGGCACTGTGGAGAAATAGGAGGCATTCCCTCCCT
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGCTCGGAGAAATTGACCOGCAACGCTGGGCACTCTCTAGAAAAAGCCAAAAGAATT CTGCTAGGAGAAATTGACCCACAACATCTGGGGCACTGTGGAGAAAGCTAAAAGATG
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGTGCCAAAAAGCAAGAAAATTCCACAGTAAAGCCAGTGCCACTTGGCTGTTCCCTCG CTATGCCAGACAAGCGAGAAANATTCCACAGTGTGGCCACCCOCAGTGGCTACCCAACTCC
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGAACTCACTGACCGAGAAAAGGATGCTCTGGCATGTTCCAGATGAGAAATTCA CAAAACATACTGGTGAAGAAGACGATTOCTCAGGCATGCTCGCTCTACATGAGGAATTAA
rat_cDNA human_5+3_corrected mus_cDNA_5	TGGTTCTGAAACTAAGGCTCTGGTGTCCAGGAAGCTCACCAACTGCTGACTCTGGAC TGGTCCCGGCCACTTAAGCMTGAACTTCCAGCAAGGACAGTGACTGCTGACTCCAGAA
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGTAATCTGGTTTATGACGAGATAGCTCTGGCACAGAAGTCTCAGCTGTGATC CAATATCTGATAGTCATGACAACATAAAATTATGGCACAGAAGCTCCTGGTGTGATT
rat_cDNA human_5+3_corrected mus_cDNA_5	CACAAACCTACATCTGAGCACCTTCCTGATTCAAATTATTTAGTGTAAACAAAGCTA CACAAATACTACCACCTGAAGAACCCACAGATTTCAACTGTCTACTGCTTAATAAACTA
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGCTGTGACAAAGAGTATGAACCCATCCATAGCAAGCAAAATAGAAGATAACACCA CAGCCATGTCAAAGATATAACCCACCATGTCAAGCCTAAATCAAGGCAACCRATC
rat_cDNA human_5+3_corrected mus_cDNA_5	AAAACCCATCAATTATCTTCCATC-----AGTAGCTGAAATTGGAGATCTG-CT AACATTCATCCACTGTCTTCCACTGCTACTTGGAGCACTGAAATTTCAGGACTCTGACA

rat_cdna	GAGGCA	--GGAAGAGACATCTTCCCAAAGTGCACACCCCTGTAAACAGGGGAAACATGGCT
human_5+3_corrected	GAGGGAAAGAGAAGAGCATTTC	--AGTA-ACCCCCAATAACAGTAAGGACTATGATC
mus_cdna_5		
rat_cdna	ACCTATGCCATACCAACACATA	--TAGTAGCTTACCCAGCAAAGCCAGTACAGTCTTGC
human_5+3_corrected	AAAGATGNTCAATGTCAAANATGCT	--TAGTAGCACCCACCAACAAA-CTATTA-----TTAG
mus_cdna_5		
rat_cdna	AGCCAATAATCCAACAGAAAGTTATGGACCTCAGATAACCTATTACAGGAGTCAGCAGAC	
human_5+3_corrected	AGTCAGTAATAACCACAAATAGTCAT	--CAGACATCTGTAAGAGAAGTGTAGTGAAC
mus_cdna_5		
rat_cdna	CTAGCAGTAGTGACATCTCTTC	--CACACTACTGCAAGACCCCTAGCTTCTCCAGTCACCCCT
human_5+3_corrected	CCAGGCACATCATCTCTT	--CACACTACTCAAAATACTTAGCACCTCCACGTCCCTT
mus_cdna_5		
rat_cdna	CAGGTTCAACACACCAGTCCTCGTCTTATTTCACATTOCTAGAAACAACAATACAGGTA	
human_5+3_corrected	CAGATCCACACACAGCTGCTCATCTCAGTTCOGATCCCTAGANNAATAGTACAGTTA	
mus_cdna_5		
rat_cdna	ACTTCCCTTGTCCAGGCACTTGGGAAGAGAGAGGACAATTGGAGCAGAGGGAGAGTTA	
human_5+3_corrected	ACATCCCCGTGTTCAAGACGCTTGGGAGGCAGAGGAAATTGGCGAAGGGGGGGGATTA	
mus_cdna_5		
rat_cdna	AAAACCCATAGAACCCCACTCTCGACGGCATAGACACAGGACTGTGAGGCCAGCAA	
human_5+3_corrected	TCAAGCCATATAGAACTCCAGTCTGCGACGGCATAGATAACAGCATTTTCAGGTCAACRA	
mus_cdna_5		
rat_cdna	TCAAGGGACCTGCTAACAAAAATGTGAGCCAAGTCCAGGCCACAGAGTACCCCTGGGATGT	
human_5+3_corrected	CCAGAGGTCTTCCTGAAAGCACTACTGCAATTCTCAGGCCACAGTGGCTCATGTGACAT	
mus_cdna_5		
rat_cdna	GCCACACATGTCTTCCGCAAGGGGCTCACAGTGGCTACTGCAAGCACTGTCAGITCCRA	
human_5+3_corrected	GTCTGTCCTGTCCTCCCACGGAGAGGCTCACCACTGCCACAGCAGCATTTCTTICCAA	
mus_cdna_5		
rat_cdna	GTTCACTCCACAGTGCCCTCCCAAACATAATAATGTTGGGTCTAGCAGAAGACTCTA	
human_5+3_corrected	GTGCGCTCCCATCACCTTCCCAAAGCTGACATTGCTAGACTCCCATCAGAAGACTCTA	
mus_cdna_5		
rat_cdna	CCACATGGTCAGAACACCAGTGTACTATTTAAGGACAAACAAATGTAGATATTGAGA	
human_5+3_corrected	CAACTCTAGTCAGAAATCCATATTACTACTCTGAGAACAAACCACTGTAGANNNNGAAA	
mus_cdna_5		
rat_cdna	TAATAACAAACCACTACAAAAATTCCGGAGGGGAAAGTAACCACGTGATTCTCACCGAAG	
human_5+3_corrected	NNACAAACACCCACAATAAAATTTCAGGACTNGAAATTCCCAAGTGAATCCAACCTGGTG	
mus_cdna_5		
rat_cdna	CAAGCATGACTTCTGCTCCAACATCTGTATCCCTGGGAAATCTCTGTAGACAATAGTG	
human_5+3_corrected	CACTCATGACATATGCTOAAACATCCATACCCATGGAAAAACTCACAAAGTAACAGCCA	
mus_cdna_5		
rat_cdna	GTCACCTGAGCATGCTGGACCACATCCAAACTGGGAAAGATTCACTGGAACACACAC	
human_5+3_corrected	GTACCCACCGTGTCTAGCACCAATGAAGCTAAAAGAGATTCACTGATTACATGTCAC	
mus_cdna_5		

rat_cdna	TTC	CCGCCCCCTCAGCACCCCCCAATACCAA-----CAAGCRAAAATTCTCAAAGA
human_5+3_corrected	TTT	CAGGTGCTATCACCAAGCCACCATGACTATTATAGCCATTACAAGGTTTCAAAGAA
<u>mus_cdna_5</u>		
rat_cdna	GGAAA	AACTCCCTGGCACAGAACITTTGTAATAACCATACOCAAAAGGCAGTTAAGGA
human_5+3_corrected	GGAAA	AACTCCCTGGCACAGAACITTTGTAATAACCATACOCAAAAGGCAGTTAAGGA
<u>mus_cdna_5</u>		
rat_cdna	ATCC	CATATCAATTGGTTACAAAAGAACCCAGCOGCCAAGGTTCCCAAATAGCTCTC
human_5+3_corrected	ATCA	ACATAAGTTAGTTACAAAAAGCAGCTGTGCTTCTAAACATCTCTG
<u>mus_cdna_5</u>		
rat_cdna	TTTT	ACCCACAG-GTCAGAGTTCCCCCTCAGATTCTACAACTCTCTGACAAGTCGCGCA
human_5+3_corrected	CTTT	ACAGAGACAGAGTTCCCCCTTCCATTTCACCACACTTCAACAAGTGTGATG
<u>mus_cdna_5</u>		
rat_cdna	CCAGC	TCTGTCTACAAACATGGCTGCCACTCAGAACRAGGGCACTGAAGTAGTATCAGGT
human_5+3_corrected	CAAAT	TCATCTAACACCTTGACTACGGCTACCCACACTACGGACAAA--ACACACAA-T
<u>mus_cdna_5</u>		
rat_cdna	GCCAG	AAGTCTCTCAGCAGGGAAAGAACAGGCCCTTCACCAACTCCTCTCCAG-TGCTCC
human_5+3_corrected	CCTGG	AAGTCTCCAACAAAGAAGGAGCTTCCCTTC-CCACCCCTAACCCATATGCTTCC
<u>mus_cdna_5</u>		
rat_cdna	TAGC	ACCTTAAGCAGAGATCTAACATACATTAAACITCTTGTCAACGGAAACCCCCACAGT
human_5+3_corrected	TAGT	TATTATAAGCARAGACTCAGTACAAAAGCATCATATCAACGCAAACAGCRACOGC
<u>mus_cdna_5</u>		
rat_cdna	GACA	AGTCTACTGCTACTGCATCTGCATTATGTTGAAACCAACGCAACAGATCCRA
human_5+3_corrected	AACA	ACTCTACCTTCCCTGCATCTGCATCTCACATTGAAACCAACAGAGAGACTCTAG
<u>mus_cdna_5</u>		
rat_cdna	AGARG	CAAAAGACCAAATTAAGGGGCTCG---GAAGAACGAAACACGCACACCCAC
human_5+3_corrected	AGCA	AAACAAATACAAAGAGAAGGACCTGAAAGAACGGACTGACCCAAACATCTC
<u>mus_cdna_5</u>		
rat_cdna	CCCCA	GGGGTTCTGGCTATAGTGCCTACTCAGCTCTAACACAGCTGATAACCCCTT
human_5+3_corrected	TOCA	AGGAGTTCTGGCTTCTACCCACTGCTATGAGAACCTCTTNGCTINNN
<u>mus_cdna_5</u>		
rat_cdna	GGCT	TTCACTCAITCCCAAGACAAAGTGTGGTGGAAATGTAAGTGCAGTTGCCTATCA
human_5+3_corrected	NGCAT	TTCACTCAITCCCAAGACAAAGTGTGGTGGAAATGTAAGTGCAGTTGCCTATCA
<u>mus_cdna_5</u>		
rat_cdna	CTCA	ACACCTCTCTGGCCA---TAACTGAACTGTTGAG-AAGTAC---ACCCAGAC
human_5+3_corrected	TCGA	AGAAACTCTTAAATCTGACAGATGTGATTGAGAAACTGACCCAAAGCAGTACTCAGAC
<u>mus_cdna_5</u>		
rat_cdna	TTTGG	GAATACACAGCTTGGAAACAACGTTGTGAGCAAATCACAGGAGACTACCAC
human_5+3_corrected	TTTGA	AGGACACAAATGCTTCTGAAACACTTGTCCAGCAAATCACACCAAGACTACCAC
<u>mus_cdna_5</u>		
rat_cdna	ACTG	AAAGAGGCTCA---GACAC---ACCAACCAACTCCTCAGCAGTGGGGCGCCCG
human_5+3_corrected	AACT	AGGAAAGCAGCTATAGACACTCACCAACCAACATTCTGAGCAGCAGTACTCT
<u>mus_cdna_5</u>		

rat_cDNA	AGTGGCCCACTCCCTCCCCACCCCTTTTACTAAGGGTGTGGTTACAGACAGCAGAACGTAC
human_5+3_corrected	AATGOCAGTTCCOCATCTCCCCCTCCCTTACTCAGAGGCAGTTACTGACAACGTGGCGAC
<u>mus_cDNA_5</u>	
rat_cDNA	ATCAGCTTTCCAGATGACGTCAAATAGAGTGGTCACCATATACTGAATCTTCAGGCACAA
human_5+3_corrected	TCCCATTTCCGGGCTTATGACRAATACTGGTCAGGTGACGAATCCTCAGGCACAA
<u>mus_cDNA_5</u>	
rat_cDNA	TACAGATCIGCAGCAACCCCTCAGCAGAGGGCTAGCCCCAATCTGAGATCATAACTGGAAC
human_5+3_corrected	TOCNNNNNNNCA---AATGCCAAGTTCA-----CINAAATTGNGAACONNNNACTCINNN
<u>mus_cDNA_5</u>	
rat_cDNA	CACTGACTCTCCCTCTAATCTGTTCCATCCACTCTGTGCCAGCACTAAGGGTAGATAA
human_5+3_corrected	NACTTCATCTACNTCTAATCTGTTACATTCTACTCCCATGCCAGCACTAACACAGTTAA
<u>mus_cDNA_5</u>	
rat_cDNA	ACCAACGAAATTCTAAATGGAAGCCCTCTCCCTGGCCAGARORCAAATATCAGCTCAGTC
human_5+3_corrected	ATCACAGAAATTCCAATTAACCTCCATCTCCCTGGGCAAAATCCAATTGGCAGAAACC
<u>mus_cDNA_5</u>	
rat_cDNA	ATACTCGAAACCATTGAGAAGGGCAAAGGOCAGCTAAGCATGTCCCCCCTCCCTCAG
human_5+3_corrected	ATACTCAGACATTGCTGAAAGGCAAAAGGCCAGAAGTAAGCATGTGGCT-ACTACAG
<u>mus_cDNA_5</u>	
rat_cDNA	-CCTTCCAGAGGCCAGCACTCATGCTCACACTGGAATACACAGAACATGCAAGAAAAGA
human_5+3_corrected	GOCTGTCGAGGCCACCACTCTGTTTCAAGATTGGGATGGACAGAAGAACACAAAGRAGA
<u>mus_cDNA_5</u>	
rat_cDNA	GTGTTTTGATAAGAAACCTGGTCAA-RACC--CAACTTCAAACATCTGCCCTTACGTCT
human_5+3_corrected	GTGACTTTGATAAGAAACCAAGTTCAAGAAGCAACACTTCAAAACTCCCTCCCTTITGACT
<u>mus_cDNA_5</u>	
rat_cDNA	CTCTACCTAAGACTCTATTGAAAAAGCCAGAATAATTGGGGGAAAGGCTGCAAGCTTTA
human_5+3_corrected	CTTTGTCAGGTATATATTGAAAAGCCCAGGATAGTTGGGAGAAAGCTGCAAGTTTA
<u>mus_cDNA_5</u>	
rat_cDNA	CAGTTCAGCTAATTAGACCTTTCTCCCTTGAGGGCTGTTGGAGACCCACTGCCCA
human_5+3_corrected	CTATTCCAGCTAACTCAGATGCTTTCTCCCTGTGAAGCTGTTGGAAATCCCTGCCCA
<u>mus_cDNA_5</u>	
rat_cDNA	TCATCCACTGGACCAGAGTTCTCAGGANTTGAATAATCCPAGGGACACAGAAAGCC
human_5+3_corrected	CCATTCAATTGGACCAGAGTNNNNTCAAGGACTTGTATCTAAGAGGAACAGAATAGCA
<u>mus_cDNA_5</u>	
rat_cDNA	GGTTCACCGTGTCTCCCAATGGCACCTTGTCCATCCAGAGGGCTAGTATTCAAGGACCGTG
human_5+3_corrected	GGGTTCAGGTTCTCCCAATGGTACCCCTGTCCATCCAGAGGGTGGAAATTCAGGACCGCG
<u>mus_cDNA_5</u>	
rat_cDNA	GACAGTACCTG1GCTCTGCATTAACTCCACTGGCGTAGACCAATTTCATG1C1C1TTGT
human_5+3_corrected	GACAGTACTTGTGTCCGCATCCAATCTGTTGGCACAGACCAOCTCRTGTCAACCTTGT
<u>mus_cDNA_5</u>	
rat_cDNA	CTGTGGTTTTAACCGGGCAAGGATTGGACAGACATGTCAGGAGATCACAGTTCACT
human_5+3_corrected	CTGTGGTTCTATCTCCAGGATCTGGAGAGAGCTACAAAGAGATCACAGTTCACT
<u>mus_cDNA_5</u>	

rat_cDNA human_5+3_corrected mus_cDNA_5	TTGGAGTACTGTGGAACCTAAAGTGAGAGTGGAGGGTATGCCGAGGCTACGGTTTCTC CCGGAGCAGTGTGGAACGTGAGTGAGCAGAGGTAAGGCCAACAGTACAGTACCT
rat_cDNA human_5+3_corrected mus_cDNA_5	GGATACTGCAACCAAACGGTGGTCTCAGAAACGCCAAGGGAGCAGAAAGGTCTGGG GGATTCTGCACAAACCAAACAGTGTCTAGAATCATCOCAGGGAGTAGGCAGGCTGTGG
rat_cDNA human_5+3_corrected mus_cDNA_5	TAACACCTQATGGAACATGTATCATCTATAATCTGAGTCCTTATGATCGTGGTTTTACA TGACGGTGTGACGGAACATGGTCTCCACAACTCTAGTATTTATGACCGTGGCTTTACA
rat_cDNA human_5+3_corrected mus_cDNA_5	AGTGTGTGGCCAGCAACCCATCTGCCAGGATTCTGTGGTTAAAGATAACAAGTCATCA AAATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCTGTGGTTAAAGATAACAAGTCATCA
rat_cDNA human_5+3_corrected mus_cDNA_5	CAGCTCCCCGTCTATTATAGAGCRAAGAGGCAAGCCATGTTGGGTTTTAGGTGGAA CAGCACCAACCTGTATCTAGAGCRAAGAGGCAAGTCATGTAGGCACTTGGGTGAAA
rat_cDNA human_5+3_corrected mus_cDNA_5	GTTTGAAACTGCCCTGCACTGCAAAGAGGAACCTCCCAGCCTAGTGTTCACTTGGGTCTTT GTTTAAACTGCCCTGTAATGCAAAAGGAACCTCCCTAGCCAGGTTTACTGGGTCTCT
rat_cDNA human_5+3_corrected mus_cDNA_5	ATGATGGGACTGAACCTAAACCATTCGAGTTGACTCAATTCCAGATTTCCTGTATCCAA CTGATGGCACTGAAGTGAAACCTTACAGTTACCAATTGAGTTGTTCTTATTTCAA
rat_cDNA human_5+3_corrected mus_cDNA_5	ATGGAACTCTGTATATAAGAGCATGGCTCTTCAGTGAGGGGACTTATGAGTGCATTG ATGGGACTTTGTATATAAGAAACCTAGCCTCTTCAGACAGGGGACTTATGAATGCATTG
rat_cDNA human_5+3_corrected mus_cDNA_5	CCACCAGCTCTAGGGCTCAGAGAGAAGGGTAGTGATTCTACTTGCGAAGAGGGAGAGA CTACCAGTTCCACTGGTTCGGAGOGAAGAGTAGTATGCTTACATGGAAAGAGOGAGTGA
rat_cDNA human_5+3_corrected mus_cDNA_5	CAATCCOCAGGATAGAAACTGOCCTCTAGAAATGGACTGAGGTGAATTGGGTGAGAAAT CCAGCCCCAGGATAGAAAGCTGCACTCCAGAAAGGGACTGAGTGAATTGGGTGAGAAAT
rat_cDNA human_5+3_corrected mus_cDNA_5	TACTACTGAACCTGCTAGCTACTGGGATCCAAAGGCTAGAATAATCTGGAGGTGCGAT TACTACTGAACCTGCTAGCCACTGGGAGGCCAACCCCAATAATGTTGGAGGTACCAT
rat_cDNA human_5+3_corrected mus_cDNA_5	CCAAGGCCTGTCATGACCTGAGCTGGCAAGAAATGGGAGGCCAACCTCAGGCTACCCAAATG CCAAGGCCTGTCATGACCTGAGCTGGCAAGAAATGGGAGGCCAACCTCAGGCTACCCAAATG
rat_cDNA human_5+3_corrected mus_cDNA_5	GATCCCTGTTATGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGGCAA GATCCCTGTTATGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGGCAA
rat_cDNA human_5+3_corrected mus_cDNA_5	GAAACAAAATGGGAGATGACCTAGTCTGATGCATGTCGGCTGAGATTGACACCTGCGA GAAACAAAATGGGAGATGATCTGATGACAGTGTAGCTAACAGTGAAGACTGAAACCTGCGA

rat_cDNA human_5+3_corrected mus_cDNA_5	AAATTGAAAGAAGCACTATTTAAGAAGCAAGTGCCTCATGGAAAGATTTCCAAAGTTC AAATTGACACAAGCACTATTTAAGAAGCAAGTGCCTCATGGAAAGATTTCCAAAGTAG
rat_cDNA human_5+3_corrected mus_cDNA_5	ACTGCAAGGCCCTCGGCTCCCTGIGCCTGAGGTATCTGGAGTTTGCTGATGGACAG ATTGCAAGCTCCGGCTCCCTGAGGTGACAGAGATACTTGGAGTTTGCTGATGGACCA
rat_cDNA human_5+3_corrected mus_cDNA_5	TGCTCAACAAATGTAGCCAAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCC TGATCAACAAATGCAATGCAAGCCGATGACAGTGGCACAGGACTAGGAGATAACCC
rat_cDNA human_5+3_corrected mus_cDNA_5	TCCACAATGGAACCTTGATTTCAACAACGTTGGATGGCAGAGGAAGGAGTTATATCT TCAACAATGGAACCTTATACTTCACAACAAAGITGGGTAGGGAGGGAGTTATACCTT
rat_cDNA human_5+3_corrected mus_cDNA_5	GCTCTGCCAGAACACCTTAGGAAAGATGAGATGAAAGTCCACCTAACAGTTCTAACAG GCTATGCCAGAACACCTTAGGAAAGATGAAATGAAAGGTCCACCTAACAGTTAACAG
rat_cDNA human_5+3_corrected mus_cDNA_5	CCATCCCACGGATAAGGAAACGCTACAGACCACATGAGGCTCAGGGCTGGAGAACAG CTGCTCCCCGATAAGGAGAGTAACAAAACCAACAGAGAAATCTAACAGTGGAGAACAG
rat_cDNA human_5+3_corrected mus_cDNA_5	CTGTCCTTGACTGCGAGGTCACTGGGAACCGAACCCAAATGTATTTGGTTGCTGCCTT CTGTCCTTGACTGCGAGGTCACTGGGAACCCAAACCAAAATATTTGGTTGCTGCCTT
rat_cDNA human_5+3_corrected mus_cDNA_5	CCAACAATGTCATTTCAATTCTCAATGACAGGTTACATTTCACTGCCAATAGAACCTTGT CCAATGACATGATTTCTCTCAATTGATAGGTACACATTTCACTGCCAATGGTCTTTGA
rat_cDNA human_5+3_corrected mus_cDNA_5	CCATCCATAAAGTGAACACACTTGACTCTGGGACTATGTGTGCGTAGCTCAGAACCTA CCATCAACAAAGTGAACACTGCTGATCTGGAGAGTACSTATGTGTAGCOOCAAATCCCA
rat_cDNA human_5+3_corrected mus_cDNA_5	GTGGGGATGACACTAAAGACATACAAACTGGACATTGTCCTCTAAACCTCCATTATCAATG GTGGGGATGACACCAAAATGTACAACACTGGATGTGGTCCTCTAAACCTCCATTATCAATG
rat_cDNA human_5+3_corrected mus_cDNA_5	GCCTGTATGCAACAAAGACTGTTATTAAGCCACAGGCCATTGGCACTCCAAAAAAACT GCCTGTATACAAACAGAACTGTTATTAAGCCACAGCTGTGAGAACATTCACAAAAAAACT
rat_cDNA human_5+3_corrected mus_cDNA_5	TTGACTGCAGAGCAGATGGGATCCCATCTTCCCAAGGTCACTGTTGGAAATGCCAGGCAATA TTGACTGCAGAGCTGAAGGACACCCATCTCTGAAGTCACTGTTGGATCACTGCCAGGCAATA
rat_cDNA human_5+3_corrected mus_cDNA_5	TTTCCCTCCAGCTCCATCTTGGAGAGCTACGGTOCATCCAAATGGAAACCTTGG TTTCCCTCCAGCOCCTACATATGAAAGCAGAGAACACAGTOCATAAAAATGGAAACCTTGG
rat_cDNA human_5+3_corrected mus_cDNA_5	AGATGAGGAACCTCCGGCTTCTGACTCTGGGACTTCAGATTCAAGCCACCTTATCTGTGTTGGGGAGGAG AAATTAGGAATGTGAGGCTTCAGATTCAAGCCACCTTATCTGTGTTGGGGAGAATGAAG

rat_cDNA	GAGGAGAGAGTGTGTGGTAGTCAGTTAGAAGTCTAGAAATGCTGAGAAGACCAACAT
human_5+3_corrected	GTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT
mus_cDNA_5	
rat_cDNA	TCAGAAACCCATTCAACGAAAAAGTCATGCCAACGCTGGCAAGCCGTAAGCAGTGAACAT
human_5+3_corrected	TTAGAAATCCATTAAATGAAAATAGTTGCCAGCTGGAAAGTCCACAGCTTGAAATT
mus_cDNA_5	
rat_cDNA	GCTCTGTGGATGGGAAACCCCCCACCTGAAATTACCTGGATCTTACCTGAOGGCACACAGAT
human_5+3_corrected	GCTCTGTGTGGTAACCCACCCACCTGAAATAATCTGGATTTACCAAATGGCACACGAT
mus_cDNA_5	
rat_cDNA	TTGCTAACAGACCACACAATTCCCCGTACTGATGGCAGGCAATGGCTCTCATCTTT
human_5+3_corrected	TTTCATGGACCACAAAGTTACAGTATCTGATAGCAAGCAATGGTTCTTTATCATTT
mus_cDNA_5	
rat_cDNA	ACAAAGCAACTCGAACAAAGTCAGGAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT
human_5+3_corrected	CTAAACAACTCGGAGATGCAGGAAATAATCGCTGTGCAGCTAGGAATAAAGGTTGGCT
mus_cDNA_5	
rat_cDNA	ACATCGAGAAACTCATCCGTAGAGATTGGGCAGAAGCCAGTCATTCTGACATAACGAAAC
human_5+3_corrected	ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAGCCAGTTATCTTACCTATGCCAC
mus_cDNA_5	
rat_cDNA	CAGGGATGGTGAAGAGCGTCAGTGGGGAAACGTTATCACTGCATTGGCTCTGTGTGGGA
human_5+3_corrected	CAGGGACAGTAAAGGCATCACTGGAGAAATCTCTATCACTGCATTGGCTCTGTGTGGGA
mus_cDNA_5	
rat_cDNA	TCCCCAAGCCAATGTCAGTGGACTAACCGGGTGGCCATGTAATGACAGGCTCAAG
human_5+3_corrected	TOCTTAAGCCAATATCAATGCRCTATGCCAAGTGGCTATGAGTAAACAGGCTCAAA
mus_cDNA_5	
rat_cDNA	TGGATGGAAAAATACATACTGCATGAAAATGCCACGCTGGTCATCAAAGCAACACAGCTC
human_5+3_corrected	TTATGGGAAATACATATTGCATGACAAATGCCACCTAGTCATTAAGAAGCAACAGCTT
mus_cDNA_5	
rat_cDNA	ACGAACGAGGAATTATATCTGTAGGGCTAAACAGTGTGGCAGGGCAATTATAGCG
human_5+3_corrected	ATGACAGAGGAAACTATATCTGTAAAGGCTAAATAGTGTGGCTACACTGATTACIG
mus_cDNA_5	
rat_cDNA	TGTCAGTGTGGITGTGGCCTACCCCTCCCGAATGATAACTACCTACCCAGGAACTGG
human_5+3_corrected	TTCCAGTAATGATTGTAGCTACCCCTCCCGAATGACAATGCTCAACCCAGGATATTG
mus_cDNA_5	
rat_cDNA	TCAGGAGGACAGGGCAACCGCTGGCAGCTCCACTGTGTGGCTTGGGAATCCCAAGCCAA
human_5+3_corrected	TCACCAGGACAGGGCAGCCCTTCAGCTCCACTGTGTGGCTTGGGAATCCCAAGCCAG
mus_cDNA_5	
rat_cDNA	AAGTCACCTGGAGACGCCAAGACACTCCCTGCTCTCAAAAGCAACAGCAGAAAACCCC
human_5+3_corrected	AAATCAGATGGGAGATGCTGACCCTCCCTCTCAACGCCAAGTAAGAGAGGACAC
mus_cDNA_5	
rat_cDNA	ATAGAAGTGAAGTGCTTCACCCACAAGGTACGCTGGTCATTGAGAATCTCAAACCTCGG
human_5+3_corrected	ATGGAAGTGAAGCAGCTTCACTTACAGGTACCCCTAGTCATTGAGAATCCCAAACCTCGG
mus_cDNA_5	

rat_cDNA	ATTCGGAGTCTATAAGTGCAGAGCTCAGAACCTACCTGGGACTGATTACGCCAACCTT
human_5+3_corrected	ATTCGGGATATAACAATGCCRGCAAAGAACCCACTTGGTAGTGATTAGCAGCAACGT
mus_cDNA_5	
rat_cDNA	ACATCCAGGTACTCTGACAGGAAGGGGGAGACTAAATTCAACAGAAGTOCACATOCACA
human_5+3_corrected	ATATTCAAGTAATCTGACATGAA-----ATATAAAGTCAAACAA-----CATCTGGCA
mus_cDNA_5	
rat_cDNA	GGGTTTATTTTTGGAAAGAAGTTAACAAAGGCAGCCATAGGCATGTAAATGAGTCTGA
human_5+3_corrected	GAATTATTTTTGGAAAGAAGTTAACAAAGGCAGCCATAGGCATGTAAATGAAATTGAA
mus_cDNA_5	
rat_cDNA	ATACATTACRGTATTAATTACATGGACATGCGA--TGA---GACTTGTAAATGAA
human_5+3_corrected	ATACATTACAGTATTAATTACATGAAACATGCAAATAAAGGACTTGTAAATTAAT
mus_cDNA_5	
rat_cDNA	GCATTGTGAACGTGAA---ACCGAGCTCTG---TGGCTCTCAAACCPAAACTCTTAACCTAA
human_5+3_corrected	GCATTATGAACGTGATGATACTGATTTATTTAACATGCTCTCAAACCAAACCTTTAACCTAA
mus_cDNA_5	
rat_cDNA	GGCCTTTGATTTGCCAACAAATAAACAAACCTTAAGAGAAAAAATGATCCACTAC
human_5+3_corrected	GGCCTTTATTTGCCAACAAATAAACAAACCTTAAGAGAAAAAATGATCCACTAC
mus_cDNA_5	
rat_cDNA	GAAATAACAAACGGCTAATGCCACCTGAATTCT-CAGTAAAAAGACCTTTCTCTGGCTAAC
human_5+3_corrected	AAAATAACAAATGGCTATGTACCTGAATTTCAGTAAAAAA---TGAACCTTCTAAT
mus_cDNA_5	
rat_cDNA	AGTTGCCAGCTGCCCTCGTGTCTGGTTCCACCTATGTCAACAAACATCGCACACAGGGTGA
human_5+3_corrected	A---CCAGTTGCCCTAGTGTCCACCTCTATCAATGTTAACAGCATGGCACTCAG---A
mus_cDNA_5	
rat_cDNA	ATGGAGTCACGGGAAAGATTAAGTTTGCCTCTGGTAAATCTCAATGTACAATATTTC
human_5+3_corrected	ACAGAGACATGGAAATATTAAATCTGC-----ATCT---ATGTATAAAATTTT
mus_cDNA_5	
rat_cDNA	TGTCTGGTTATAAAACATTTC-GATAAAACGAAAAAAGAAAAAAGAAAAAAG
human_5+3_corrected	TGT---GGTTATAAAATTTCGCTAAAACCTACAGAAAAAAG
mus_cDNA_5	
rat_cDNA	AAAA
human_5+3_corrected	---
mus_cDNA_5	

(rat\_cDNA: SEQ ID NO:7)  
 (human\_5+3 corrected: SEQ ID NO:8)  
 (mus\_cDNA\_5: SEQ ID NO:9)

Figure 15

rat	MQVRGREVSGLLISLTAVCLVVTGSPACPRRCACIVPTEVHCTFRYLTSPIDGIPANVE
human_5+3_corrected	MKVKGRRGITCLLVSPAVICLVAATPGKACPRRCACIVPTEVHCTFRYLTSPIDGIPANVE
mouse_5_corrected	MOKRGREVSCLLISLTAVCLVVTGSPRVCPRRCACIVPTEVHCTFRDLTSIPD-GPANVE
rat	RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDDTFSGLQSLOVLRKMSYNKVQII
human_5+3_corrected	RINLGYNSLVRLMETDFSGLTKELEMLHSNGIHTIPDKTFSDIQALQVLKMSYNKVRL
mouse_5_corrected	RVNLGYNSLTRLTENDFSGLSRLEELMLHSNGIHRVSDDTFSGLQSLOVLRKMSYNKVQII
rat	RKDTFYGLGSILVRLLHLDNNIEFINPEAFYGLTSLRVHLEGNRLTKLHPDTFVSLSYLQ
human_5+3_corrected	QKDTFYGLRSLTRLHMDNNIEFINPEVFYGLNFLRVHLEGNQLTKLHPDTFVSLSYLQ
mouse_5_corrected	EKDTLYGLRSLTRLHLDNNIEFINPEAFYGLTLLRVHLEGNRLTKLHPDTFVSLSYLQ
rat	IFKTSPIKYLFLSDNF-TSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWQGNPDI
human_5+3_corrected	IFKISPIKFLYLSDNFLTSLPQEMVSYMPDLSOISLYLHGNPWTCDCHLKWLSDWIQ--PDV
mouse_5_corrected	IFKTSPIKKLYLYDNF-TSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWQGNP--
rat	IKCKKDRSSSSPQQCPLCMNPRI SKGRPFAMVPSGAFLCTKPTIDPSLKSKSLSVTOEDNG
human_5+3_corrected	IKCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAFAQCKPTIDSSLKSKSLSILEDSS
mouse_5_corrected	-----
rat	SASTSPQDFIEPFGSLSLNMTXISGNXADMVCSTIQKPSRTSPTAFTEENDYIMINASPST
human_5+3_corrected	SAFISPQGEMAPFGSILTINMTDQSGNEAMVCSTIQKPSRTSPIAFTEENDYIVINTSFST
mouse_5_corrected	-----
rat	NLVCSDYDHIQPVWQILALYSDSPLIILERKPQLTETPSLSSRYKQVALRPEDIFTSIEA
human_5+3_corrected	FLVCNDIDYGHIQPVWQILALYSDSPLIERSHLLSETPQLYYYKQVAPKPEDIFTNIEA
mouse_5_corrected	-----
rat	DVRADPFWFQQEKTIVLQLNRATTTLSTLQIOPFSTDAQIALPRAEMRAERLKWTMILMMNN
human_5+3_corrected	DLRADPSWLMQDQISLQLNRATTFTSTLQIOPYSSDAQITLPRAEMLPVHKWTMISRDNN
mouse_5_corrected	-----
rat	PKLERTVLVGGTIALSCP GKGDPSPHLENLLADGSKVRAPYVSEDGRILIDRKNGKLELOM
human_5+3_corrected	TKLEHTVLVGGTVGLNCPGQGDPTPHDVWLLADGSKVRAPYVSEDGRILIDRKNGKLELOM
mouse_5_corrected	-----
rat	ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDGVQHVVGETLDLPCLSSTGV
human_5+3_corrected	ADSFDGTGVYHCISSNYDDADILTYRITVVEPLVAYQENGIIHHTVFIGETLDLPCHSSTGI
mouse_5_corrected	-----
rat	PDASISWILPGNTIVFSQPSRDRQIILNNGTIRLILQVTPKDOGHYOCVAANPSGADFSSFKV
human_5+3_corrected	PDASISWIPGNNVLYQSSRDKVVLNNGTIRLILQVTPKDOGHYRCVAANPSGVDFLIQPV
mouse_5_corrected	-----
rat	SVQKKQRMVEHDREAGGSGLGEPNSSVSLKQPAISLKL SASALTGSEAGKROVSGVHREK NK
human_5+3_corrected	SVRMKGQRPLEHDGETEGSGLDESPNIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRHN
mouse_5_corrected	-----
rat	HRDLIIRRGGDSTLRRFREHRRQLPLSARRIDPQRWAALLEKAKRNSEVPKQENTTVKPV
human_5+3_corrected	YRELTQRRGGDSTLRRFRENRRHFFPSARRIDPQRWAALLEKAKRNAMPDKRENTTVSPP
mouse_5_corrected	-----

rat	PLAVPLVELTDEEKDASGMIPPDEEPVVLTKASGVPGRSPTADSGPVNHCMTS1ASGT
human_5+3_corrected	PVVTOLPNP1GEEEDDSQMLALHEEMVPAKALNLPARTVTADSR1ISDPMTNINYGT
mouse_5_corrected	
rat	EVS-TVNPOQTLQSEHLPDFKLFSVTINGTAVTKSMNPSIASKIEDTTNQNPIIIIFP--SV
human_5+3_corrected	EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHS3TVFPILLGA
mouse_5_corrected	
rat	AETRDSAQAGRAS--SQSAHPVTGGNMAFYGHNTTYSSFTSKASTVLOPINPTESYGPQI
human_5+3_corrected	TEFQDSDQMRGRHFFQSRRPITVRTMIKVNVKMLSSTTNKL--LLESVNTTNSH--QT
mouse_5_corrected	
rat	PTIGV6RPSSSDISSETTADPFSHSPSGSHTTASSLFHIPRNNTGNPPLSRHLGRERT
human_5+3_corrected	SVREVSEPREHNHFY3HTQ1LSTTFPSDPHTAHSQFPIPRNS-TVNIPLERFGRQRK
mouse_5_corrected	
rat	IWSRGRVENPHRTPVIRRHRHRTVRPAIKGPANKVSVQVPATEYPMCHTCPSAEGLTVA
human_5+3_corrected	IGGRGRIISPYRTPVIRBHRYSIFRSTTRGSSEKTTAFSATVINVTCLSCLPRERLTTA
mouse_5_corrected	
rat	TAALSVPSSSSALPKNNVGVIAEESTTVVKKPLLFDKDNVDIEIITTTTKYSGGES
human_5+3_corrected	TAALSFPSAAPITFKADIARVESEESTLVQNPLLLENKF-SVEKTTPTIKYPRTEI
mouse_5_corrected	
rat	NHVIPTEASMTSAPTSVSLGKSPVDMNSGHLSPGTTQTCRDSVETPLPSPLSTP--SIP
human_5+3_corrected	SQVTPGAVMTYAPTSIPMEKTHKVNASYPRVSS3TNEAKRDSVITSSLGAITKPPMTII
mouse_5_corrected	
rat	TSTKFSKRKTPLEHQIFVNNOKEGMLKNPYQFGLOKNPAAKLPKIAFLPTGQSSPSDST
human_5+3_corrected	ATLRFSSRKIPWQONFVNHHNFKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFT
mouse_5_corrected	
rat	TLLTSPPPALSTTMAATONKGTEVVSGARSLSACKQ-PFTNSSPVLPSLTICKRSNTLNF
human_5+3_corrected	TISTSVMOIPSNLTTAHTTTKTRHNG-SLPT-KKELPFPPLNPMPLPSIIISKDSSTKSI
mouse_5_corrected	
rat	LSTETPT-VTSPTATASVIMSETQRTSKEAKDQIG-P-RKQRRNNANTTPRQVSGYSAY
human_5+3_corrected	ISTQTAIPATTPTFFASVITYETQTERSRAQTIQEQQEPQKRNRTDPNISPDQSSGFTTP
mouse_5_corrected	
rat	SALTADTPFLAFSHSPRQDDGGNVSAVAYHSTTS-LIAITELFEKIQTQLGNTIALETT
human_5+3_corrected	TAMTP-PALAFTHSPPENTTGISSTISFHRSRTLNLTDVIEELAQASTOTLKSTIASETT
mouse_5_corrected	
rat	LLSKSQESTTVKRAS-DTP-PFLLSGAPPVPTPSPPPFKGVVTDISKVTSAFQMTSNRV
human_5+3_corrected	LLSKSHQSTTRKASLDTPIPPFLSSSATIMPVPISPPFQRAVTDTRGDSHEFLMTNTV
mouse_5_corrected	
rat	VTIYESSRHENTDLQOPSAEAESPNEIITGTTDSPSNLFPSTSVEALRVDKPQNSKWKPS
human_5+3_corrected	VKLHESRHN-LQMPSSOLEP-----LTSSTSNNLMSTPMBALTTVKSQNSKLTPSP
mouse_5_corrected	
rat	WPEHKYQLKSYSSETIERGKRPAVSMSPHLSLPSAETHASHBNTQKHAEKSVDKXKGQNP
human_5+3_corrected	WAEYQFWHKPYSDIAEKGKKEPEVSMIATTGLSEATLVSWDGQKNTKKSDFDKKPVOEA
mouse_5_corrected	

rat	-TSHLPYSLPKTLLKKPRIIGGKAASFTVPA	NDFLPCEAVG	GPLPIIHWTRVSSGX						
human_5+3_corrected	TSKLLPFDLSR	YIFPEKPRIVGGKAASFTIP	PANSAFLPCAVGNPLPTIHWTRVS-GL						
mouse_5_corrected									
rat	KISQGTQSRFHVLPGNTLSIQRVSIQDRGQYLCSAFNPLGVDSHFV	SLSVVFPARILD							
human_5+3_corrected	DLSRGQNQNSRVQVLPNGT	LSIQRVEIQDRGQYLCSASNLF	GTDHLHVTLSVVSYPPRIE						
mouse_5_corrected									
rat	RHVKEITVHFGSTVELKCRVEQMPPTV	WILANO	VVSETAKGSRKVWVTPDGTIIYN						
human_5+3_corrected	RTKEITVHSGSTVELKRAEGRSP	PTVWILANO	TTVSESSOGGRQAVVTVDGTLVLEN						
mouse_5_corrected									
rat	LSLYDRGFYKCVASNPGQDSLLVKIQVIAAPPV	ILEQKROAIVGVLGGSLKLPC	TAKGT						
human_5+3_corrected	LSIYDRGFYKCVASNPGQDSLLVKIQVIAAPPV	ILEQRRQVIVGTVGESLKLPC	TAKGT						
mouse_5_corrected									
rat	POPSVWVLYDGTELKPLQLTHSRF	YIYIRSIAPSVRGTYECIATSSGSERRV							
human_5+3_corrected	POPSVWVLSDGTEVKPLQFTNSKLF	FSNGTLYIRNLASSDRGTYECIATSTGSERRV							
mouse_5_corrected									
rat	VILTVEEGETIPRIETASQNTIEVN	LGEKLLLNC	SATGDPKPRIIWRRLPSKAVIDQWHRM						
human_5+3_corrected	VMLTMEERTVSPRIEAASQRT	EVNPGDK	LLLNC	SATGEPKPQIMWRRLPSKAVVDQ---					
mouse_5_corrected									
rat	GSRIVVYPNGSLVVGSVTEKDAGDYL	CVARNM	GDDILVLMHVRIRLTPAKIEQKOFKKQ						
human_5+3_corrected	GSRIVVYPNGSLFIGSVTEKDAGVY	LCVARNM	GDDILVLMHVSIRI	PAKIDHKQYERKQ					
mouse_5_corrected									
rat	VLAGKDFQVDC	KAASGSPVPEVSN	SLPDGT	VINNVQAADDG					
human_5+3_corrected	VLAGKDFQVDC	KAASGSPVPEI	SNL	GYRTKRYTLEFHNGTLYFNNV					
mouse_5_corrected				VLAGKDFQVDC	KAASGSPVPEI	SNL	PDGT	MINNAMQADDG	SRTRRYTLEFHNGTLYFNNV
rat	GVAEEGDYICSAQNTLGKDEM	KVHLTVTA	IPRIOSYCTTMR	LAGETAVLDCEVTGEP					
human_5+3_corrected	GVAEEGDYICSAQNTLGKDEM	KVHLTVTA	IPRIOSNKTKR	IKAGDTAVLDCEVTGDP					
mouse_5_corrected									
rat	KPNFWLLPSNNVISFSNDRT	PHANRTLSIHKVKPLDSD	GDYVCVAONPSGDDITKTYKLD						
human_5+3_corrected	KPKFWLLPSNDMISFSI	ORYTFHANGSLTINKVKLLD	SGEYVCVARNPSGDDATKMYKLD						
mouse_5_corrected									
rat	IVSKPPLINGLYANKTVIKATAIRHS	KKYFDCRADGIPSSOVTWIMP	GNIFLPAPYFGSR						
human_5+3_corrected	IVSKPPLINGLYTNRTVIKATA	AVRHSKKHFD	CRAEGTPSPEVMWIMP	DNLFLTAPYGSR					
mouse_5_corrected									
rat	VTVHPNGTLEMNRNIRLSDADFTC	WVSEGGE	SVLVVOLEVLEMLRRPTFRNP	FNEKIVIA					
human_5+3_corrected	VTVHKNGTLEMNRVRLSDADFTC	VARNEGGE	SVLVVOLEVLEMLRRPTFRNP	FNEKIVIA					
mouse_5_corrected									
rat	QAGKPVALNCSV	DGNPPPEITWILPDGTQFANR	PANSPYIMAGNGS	LILYKATRNKGKY					
human_5+3_corrected	QLGKSTALNCSV	DGNPPPEI	IWILPNGT	RFPSNGPOSYQYLIASNGSFII					
mouse_5_corrected				SKTTREDAGKY					
rat	RCAARNKVGYIEKL	LILLEIGOKPVILTYEPGMVKS	VSGEPLSLHC	VS	SDGIPKPNVWFTTP				
human_5+3_corrected	RCAARNKVGYIEKL	VILLEIGOKPVILTYAPGTVKG	LGGBSLSLHC	VS	SDGIPKPNWIKWIMP				
mouse_5_corrected									

rat	GGHVIDRPQVDGKYILHEENGTLVIAKATAHDQNYICRAQNSVGQAVIEVSVMVVAYPPR
human_5+3_corrected	SGYVVDRPQINGKYLIEUNGTLVIAKATAYDRGNYICKAQNNSVGETLITVPVMTIVAYPPR
mouse_5_corrected	<hr/>

rat	IINYLPRNMLRRTGEANOLHCVALGIPKPKVITWETPRHSILLSKATARKPHRSEMLHPQGT
human_5+3_corrected	ITNRPPRSIVTRTGAAPQLHCVALGVPKPEITWEMPDHISLLSTASKERTHGSEQLHLQGT
mouse_5_corrected	<hr/>

rat	LVIONLQTSDSGVYKCRAQNLGLTDYATTYIQV
human_5+3_corrected	LVIONPQTSDSGIYKCTAKNPLGSDYAATTYIQV
mouse_5_corrected	<hr/>

(rat: SEQ ID NO:10)

(human\_5+3\_corrected: SEQ ID NO:11)

(mouse\_5\_corrected: SEQ ID NO:12)

Figure 16



rat human_5+3_corrected	SRIHVYPNGSLVVGSVTEKDAGDYLCVARKMGDDLVIMHVRRLTPAKIEQKQYFKKQV SWIHVYPNGSLFIGSVTEKDAGSYLICVARKMGDDLVIMHVSRLKPAKIDHKQYFRKQV *****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	LHGKDFQVDCKASGSPVPEVWSLPGTVLNNVAQADDSGYRTKRYTLEFHNGTLYFNNG LHGKDFQVDCKASGSPVPEIWSLPGTMINNAMQADDSGHTRRYTLEFHNGTLYENKVG *****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	MAEEGDYICSQANTLGKDEMVKHLTVLTAIPRQSYKTTMRLRAGETAVLDCEVTGEPK VAEEGDYTCYAQNTLGKDEMVKHLTVITAAPRQSYKTKRKAQDTAVLDCEVTGDPK ***** * *****;*****;***** ** . *;*;*****;*****;**
rat human_5+3_corrected	PNVFWLLPSNNVISFSNDRFTHANRTLSIHKVKPLDSGYVCVAQNPSGDDTKYKLDV PKIFWLLPSNDMISFSIDRYTFHANGSLTINKVLLDSEYVCVARNPSGDDTKMYKLDV *:*****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	VSKPPLLINGLYANKTVIKATAIRHSKKYFDRADGIPSSQVTWIMPQNIFLPAPYFGSRV VSKPPLILINGLYNRTVIKATAVRHSKKHFIDCRAEGTPSPFVMWIMPDNIFLTAPYYGSRI *****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	TVHPNGTLEMNRNIRLSDSADFTCVVRSEGGEVSLLVQLEVLEMLRRPTFRNPFNEKVIAQ TVHKNGTLEIRNVLSDSADFTICVARNEGGEVSLLVQLEVLEMLRRPTFRNPFNEKVIAQ *** * *;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	AGKPVALNCSDGNPPPEITWLPDGTOFANRPHNSPYLMAGNGSLLILYKATRNKSGKYL LGKSTALNCSDGNPPPEIIWLPNGTRFSNGPQSYQYLIASNGSFIIISKTREDAGKYL **..*****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	CAARNKVGYIEKLILLEIGQKPVILTYEPGMVKSVSGEPLSLHCVSDGIPKPNVKWTTPG CAARNKVGYIEKLVILLEIGQKPVILTYAPGTVKGJSGESLSSLHCVSDGIPKPNUKWTMPS *****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	GEVTDPOQVDGKYILHENGTIVIKATTAAHDQGNYICRAQNSVGQAVISVSMVVAYPPRI GYVVDPRQINGKYILHDNGTIVIKEATAVDRGNYICKAQNNSVGETLITVPVMIVAYPPRI *:*****;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	INYLPFRNMLRRIGEAMOLACVALGIPPKVWETPRHSLLSKATAKPHRSEMELHPQGTL TNRPPRSIVTRTGAFAQLNCVALGVPKPEITWEMPDHSSLSTASKERTHGSEQLHLOGTL * *.;*****;*****;*****;*****;*****;*****;*****;*****;*****;
rat human_5+3_corrected	VIONLQTSDSGVYKCRAGNLLGTDYATTYIQVL VIQNPQTSDSGTYKCTAKNPLGSDYAATYIQVI *****;*****;*****;*****;*****;

(rat: SEQ ID NO:13)  
 (human\_5+3\_corrected: SEQ ID NO:14)

Figure 17

MQKRGREVSCLLISLTACILVVTPGSRVCPRRCACYVPTEVHCTFRDLTSIPDGPANVER  
 VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLQLQVLKMSYNKVQIE  
 KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLRLVHLEGNRLTKLHPDTFVSLSYLQIF  
 KTSFIKXLYLYDNFTSLPKEMVSSMPNLESLYLHGNPWTCDCHLKWLSEWMQGNP  
 (SEQ ID NO: 15)

Figure 18

MVKGRGITCLLVSFAVICLVATPGGKACP RRCAC YMPTEVHCTFRYLTSIPDSIPP NVE  
 RINLG YNSLVR LMETDFSGLTKLELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK  
 LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL  
 QIFKISFIKFLYLSDNFLTSLPQEMS YMPDLSLLY LHGNPWTCDCHLRWLSDWI QPDVI  
 KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKS KSLTILEDSSS  
 AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEEENDYTVLNTSFSTFL  
 VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR  
 ADPSWLMQDQISLQLNRATTFSTLQIYSSDAQITLPRAEMRPVHKW TMI S RDNNNTK  
 LEHTV LVGGTVGLNC PGQGDPTPHVDWLLADGSKVRA PYVSEDGRILIDKSGKLELOM  
 ADSFDTGVYHC ISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPC HSTGIP  
 DASISWVIPGNNVLYQSSRDKKV LNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV  
 SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEGKHTSSTS KRH  
 NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHW AALLEKAKKNAMPDKRENTTV  
 SPPP VVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN  
 YGTEFSPVVNSQILPPEPTDFKLSTA ILLTAMS KNINPTMSSQIQGTTNQHSSTVFPLLL G  
 ATEFQDSDQMGRGREHFQS RPPITVRTMI DVNVKMLSSTNKLLLESVN SHQTSVREV  
 SEPRHNHFYSHTTQILSTSTFP SDPHTAAHSQFPIRNSTVNIP LFR RFGRQRKIGGRGRIIS  
 PY RTPV LRRHRY SIFRSTTRGSSEKSTTAFSATV LNV TCLS CLP RELT TATA AL SFPSA API  
 TFPKADIARV PSEESTL VQNPLLLENKPSVEKTTPTIKYFRTEISQVTPTGA VMTYAPT  
 SIPMEKTHKVNA SYPRV SSTNEAKRDSV ITSSL SGAI T KPPMTII ATRFSRRKIPWQQNFV  
 NNHNPKGRLRNQHKVSLQKSTA VMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNTLTT  
 AHHTT KTHNPGSLPTKKE LPFPPLNPM LPSIISKDSSTKSIISTQTAIPATTPTF PASVITYE  
 TQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTPTAMTPPALAFTHSPP ENTTGISST  
 ISFHSRTLNLTDVIEELAQASTQTLKSTIA SETT LSSKSHQSTTRKASLDTPIPPFLSSSAT  
 LMPVPISPPFTQRAVTDTRGDSHFR LMTNTVVKLHESSRHNLQMPSSQLEPLTSSTS NLL  
 HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGKKPEVSM LATTGLSEATTLV  
 SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDLSR YIFEKPRIVGGKAASFTIPANSDAF  
 LPCEAVGNPLPTIH WTR VSGLDLSRG NQNSRVQVLPNGTLSIQR VEI QDRFQYLC SASNL  
 FGTDHLHVTLSVSYPPRILER RTKEITVHSGSTVELKCRAEGRPSPTV TWILANQT VVSE  
 SSQGSRQA VVTVDGT LVLHNLSIYDRGFYKCVASNPGGQDSLLVKI QVIAAPPVILEQRR  
 QVIVGTWGESLKLPCA KGT P QPSVY WVL SDGTEVKPLQFTNSKLF LFSNGT LYIRNL AS

SDRFTYECIATSSTGSERR VVMLTMEER VTSPRIEAASQKRTEVNFGDKLLLNCATGEP  
 KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGYLCVARNKGDDLILMHVSLR  
 LKPAKIDHKQYFRKQVLHGKDFQVDCASGSPVPEISWSLPDGTMINNAMQADDGHR  
 TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNLTGKDEMVKHLTVITAAPRIRQSNKTN  
 KRIKAGDTAAVLDCEVTGDPKPKIFWLLPSNDMISFSIDRYTFHANGSLINKVKLLDSG  
 EYVCVARNPMSGDDTKMYKLDVVSCKPPLINGLYTNRTVIKATAVRHSKKHFDCAEGTP  
 SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGESVLVVQLE  
 VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSVDGNPPPEIWILPNGTRFSNGPQSY  
 QYLIASNGSFIISSKTTREDAGKYRCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGE  
 SLSLHCVSDGIPKPNIKWTMPSGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKA  
 QNSVGHTLITVPVMIVA YPPRITNRPPRSIVTRTGAAFQLHCVALGVPKPEITWEMPDHS  
 LLSTASKERTHGSEQLHLQGTLVIQNPQTSDSGIYKCTAKNPLGSDYAA TYIQVI (SEQ ID  
 NO: 16)

Figure 19

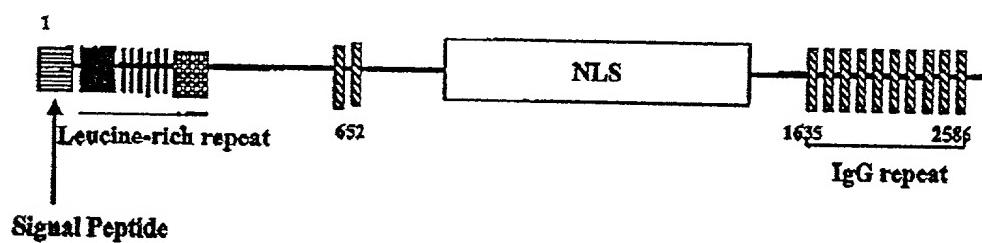


Figure 20

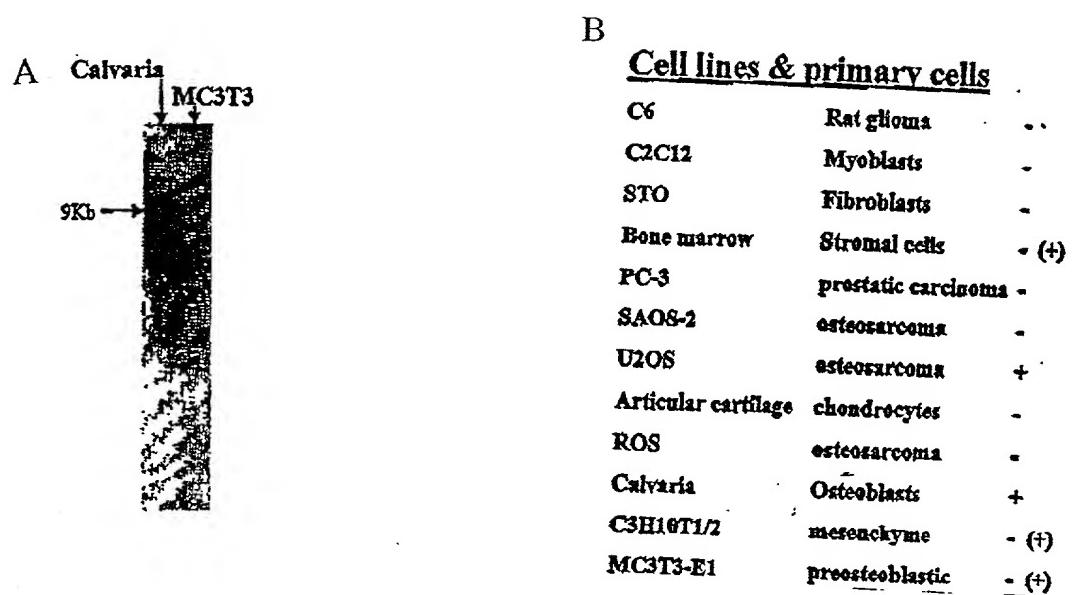
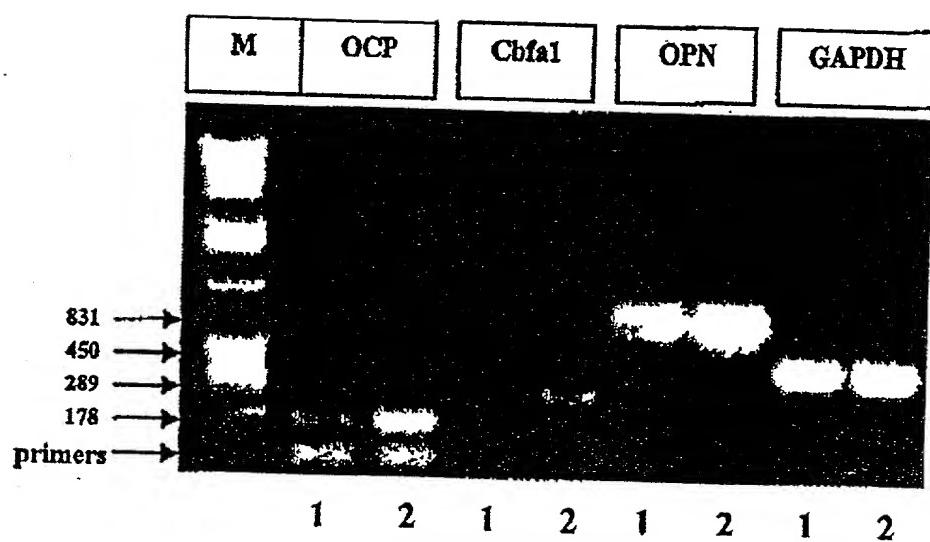


Figure 21



51/90

Figure 22

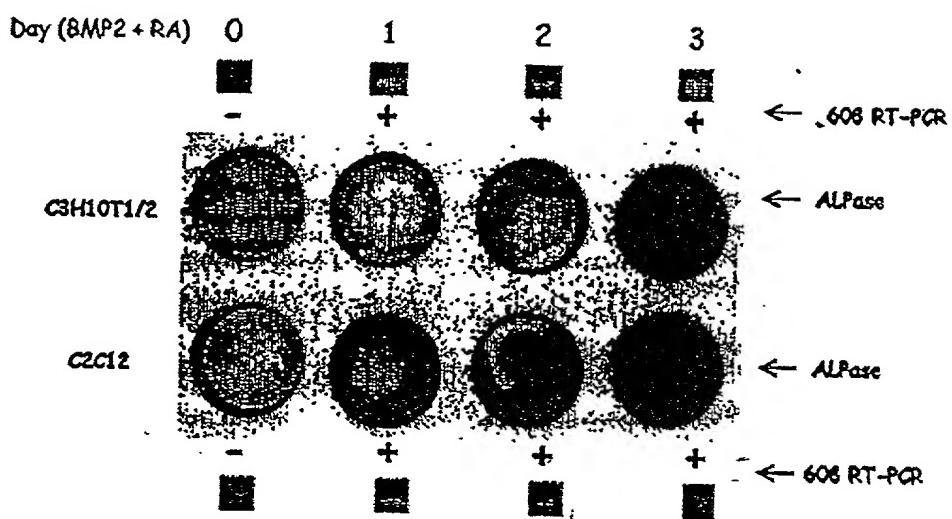
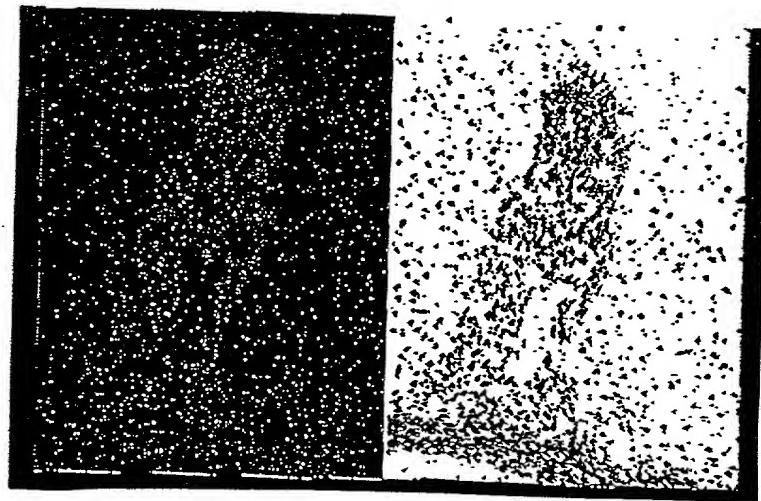


Figure 23



52/90

Figure 24

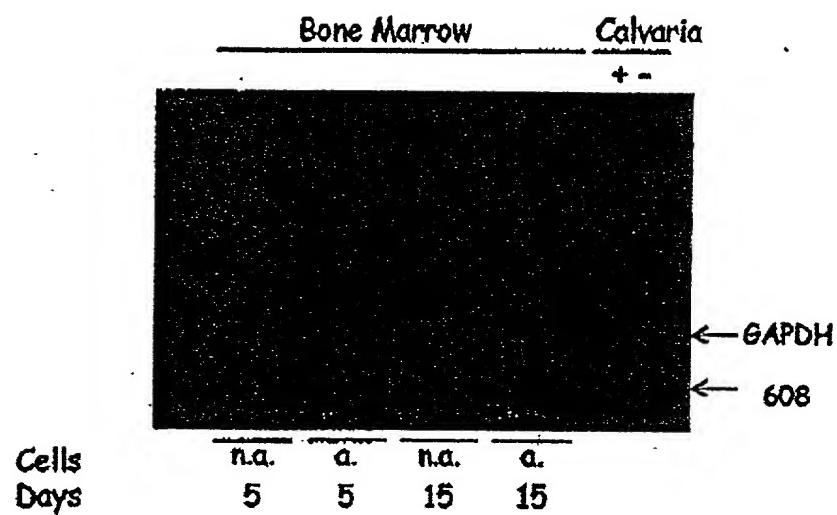
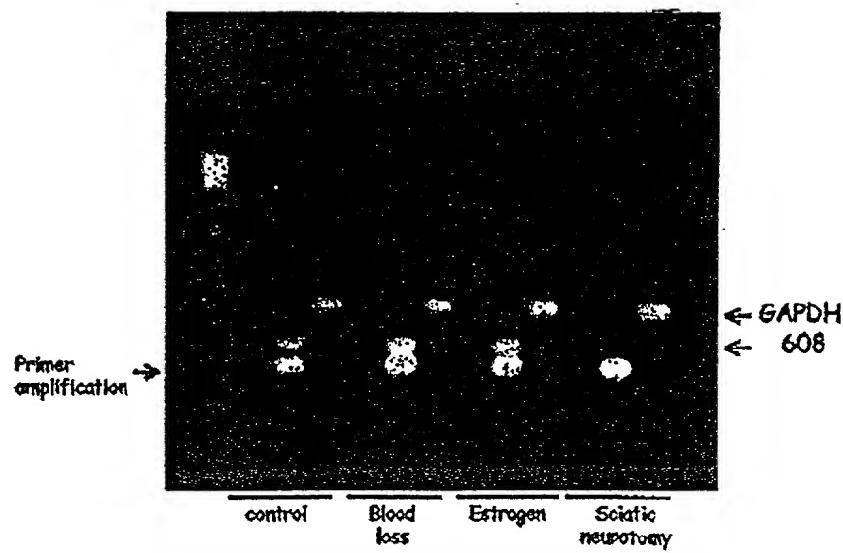


Figure 25



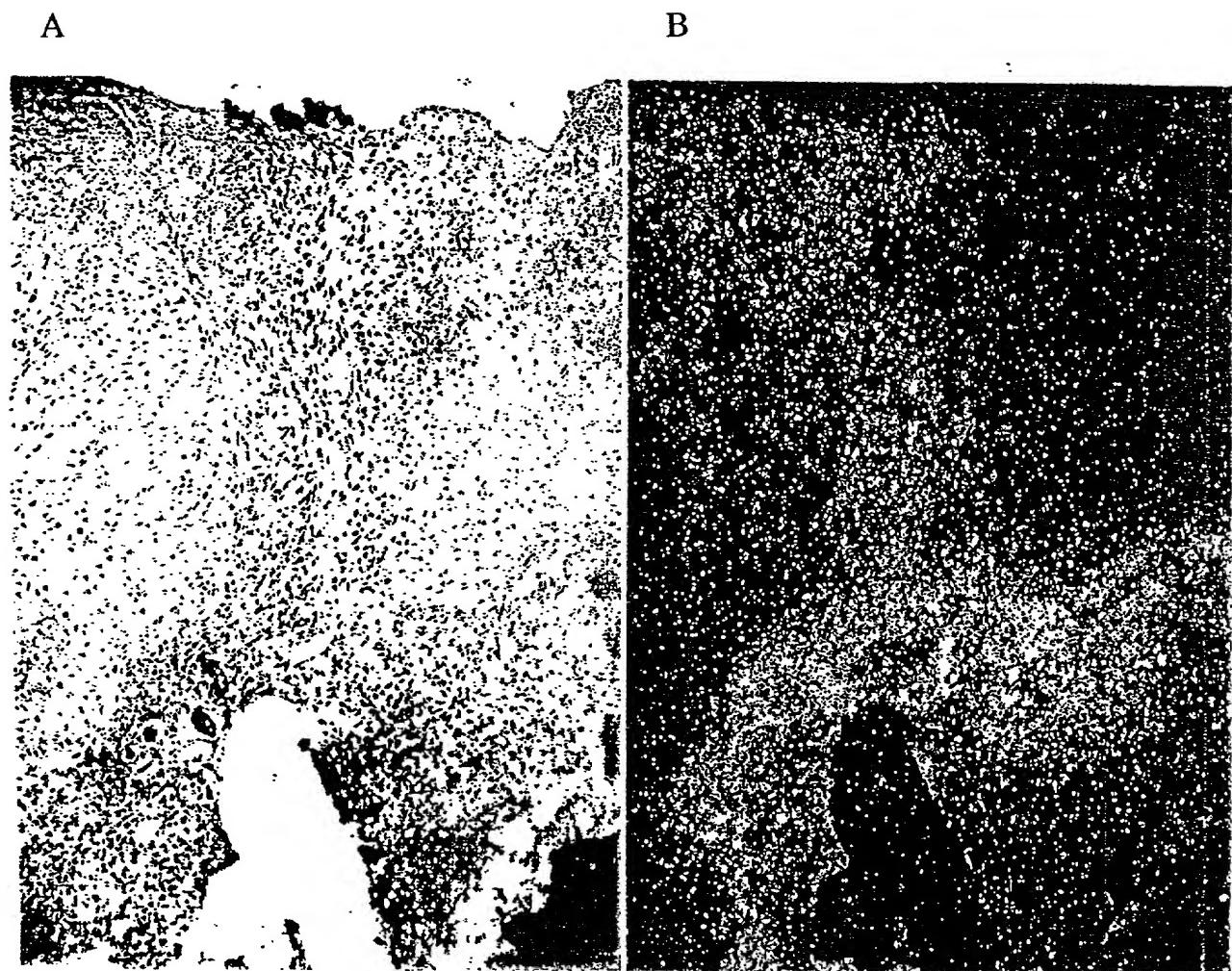
53/90

Figure 26



54/90

Figure 27

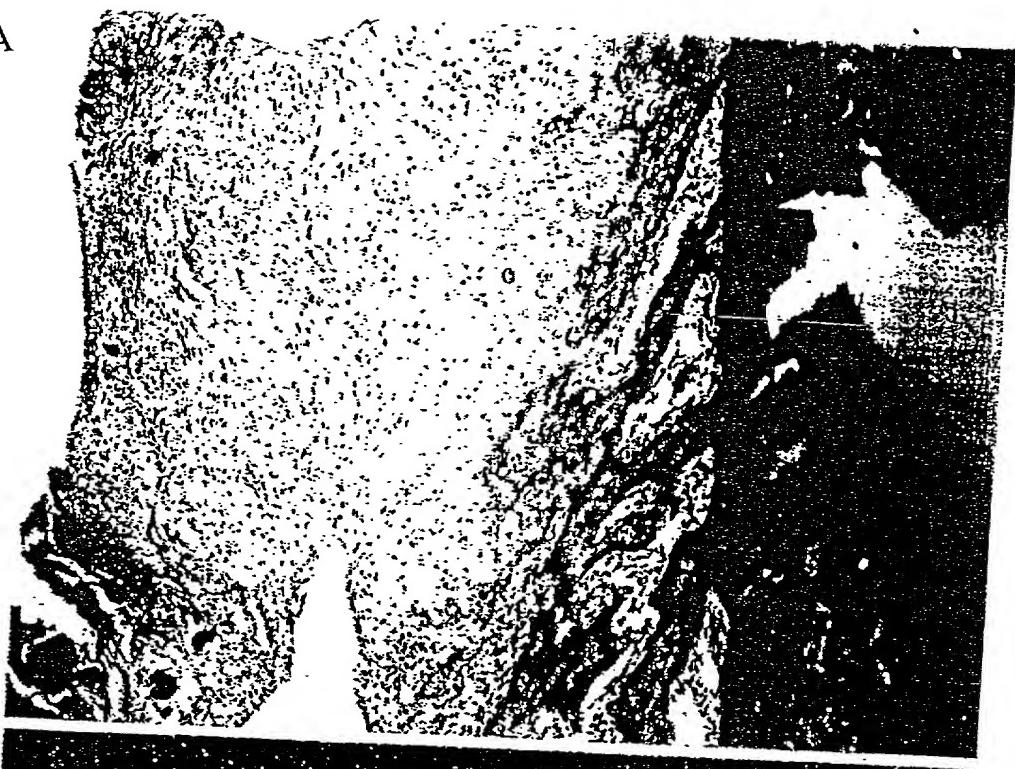


2022-07-06 09:50:00

55/90

Figure 28

A



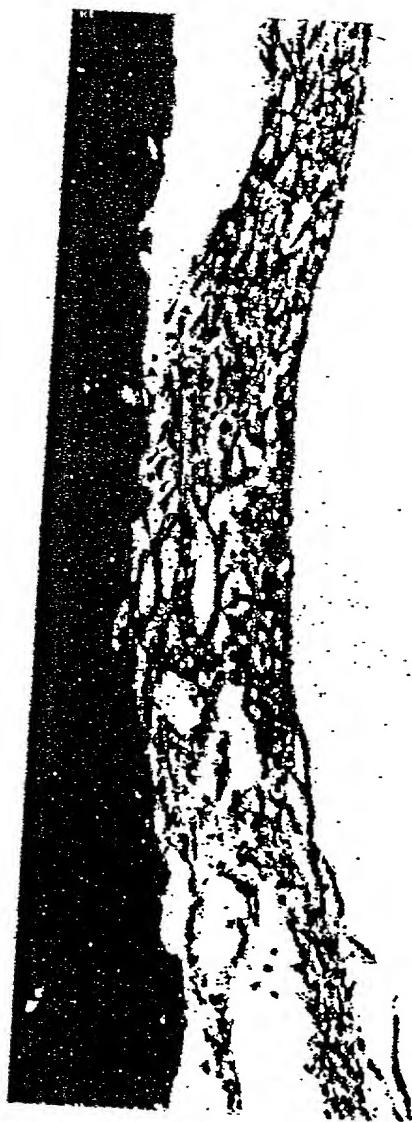
B



56/90

Figure 29

A

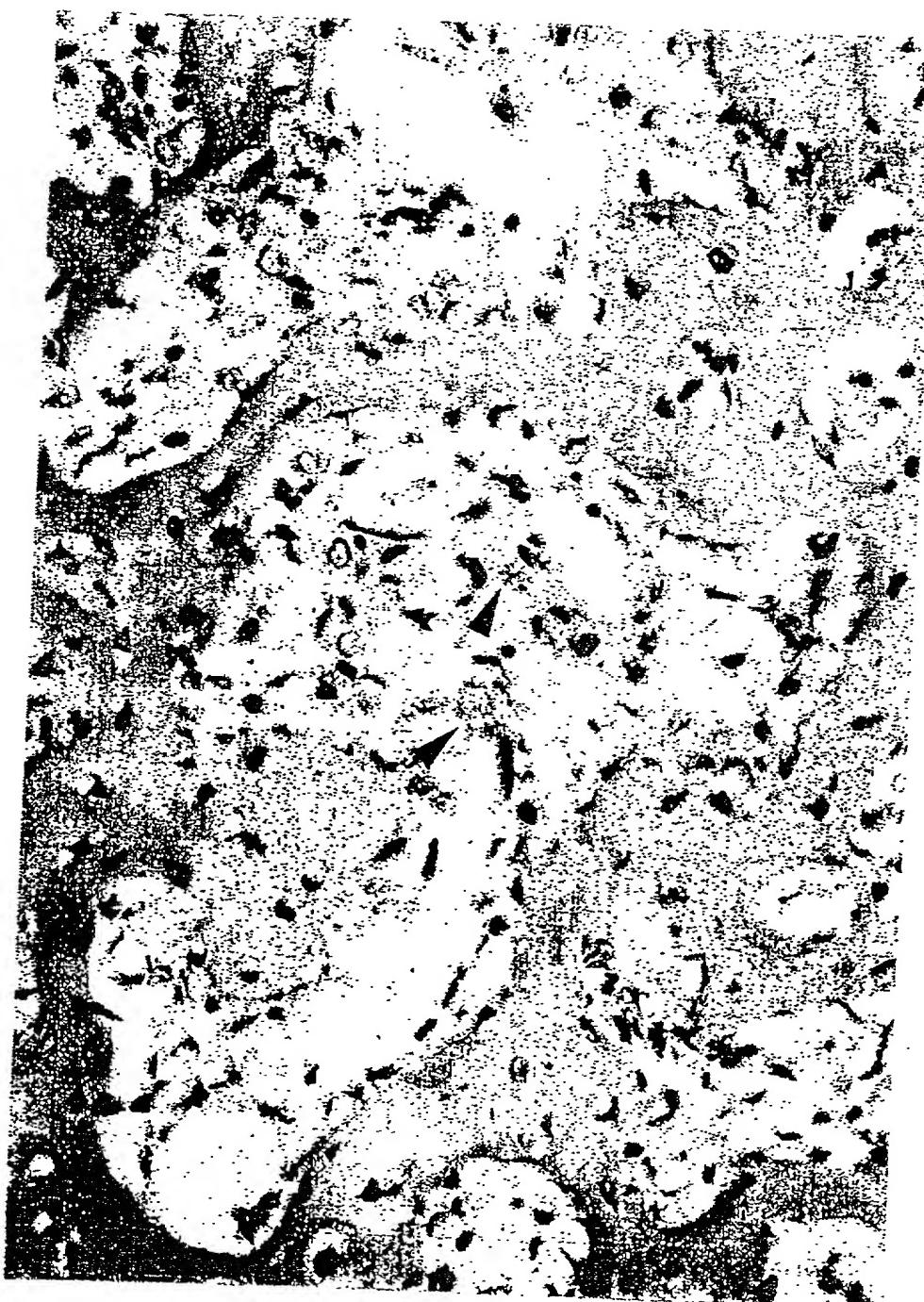


B



57/90

Figure 30



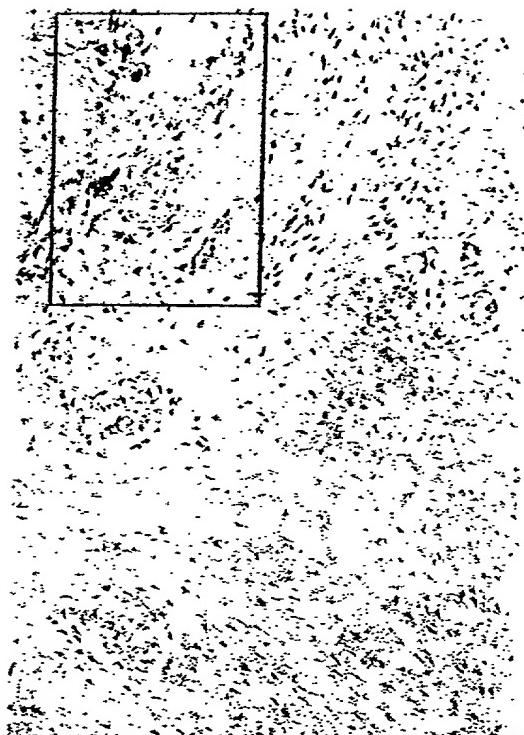
58/90

Figure 31

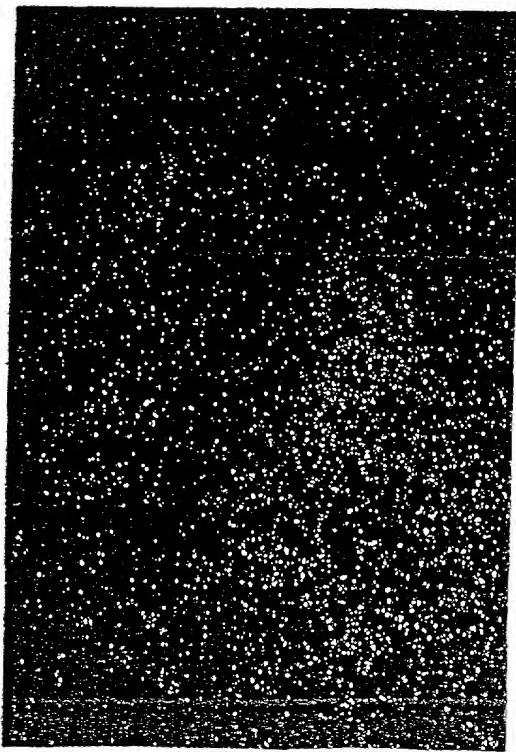


Figure 32

A

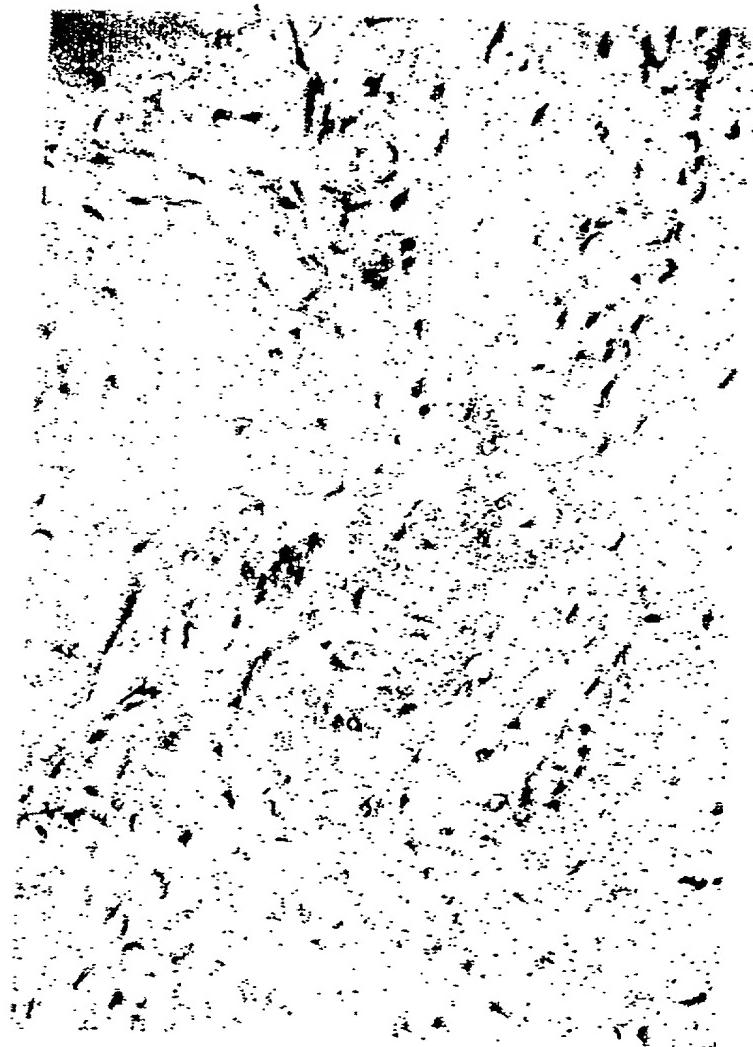


B



60/90

Figure 33



0930 1020 - 0942 022020

61/90

Figure 34

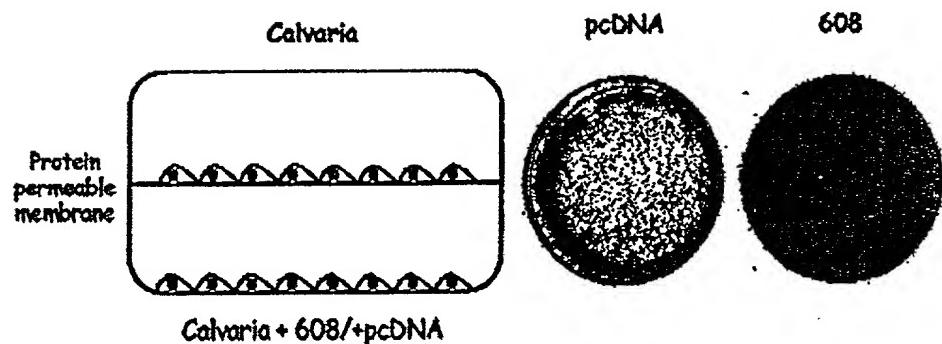
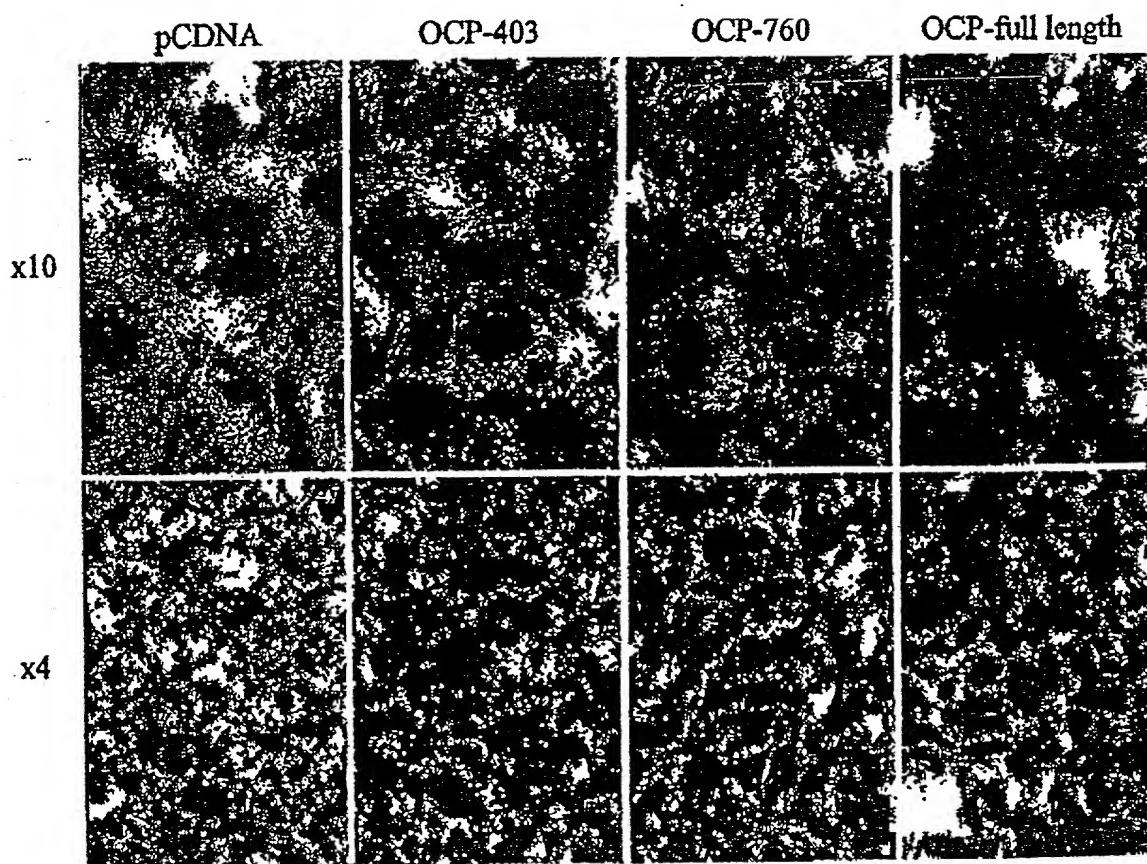


Figure 35



62/90

Figure 36

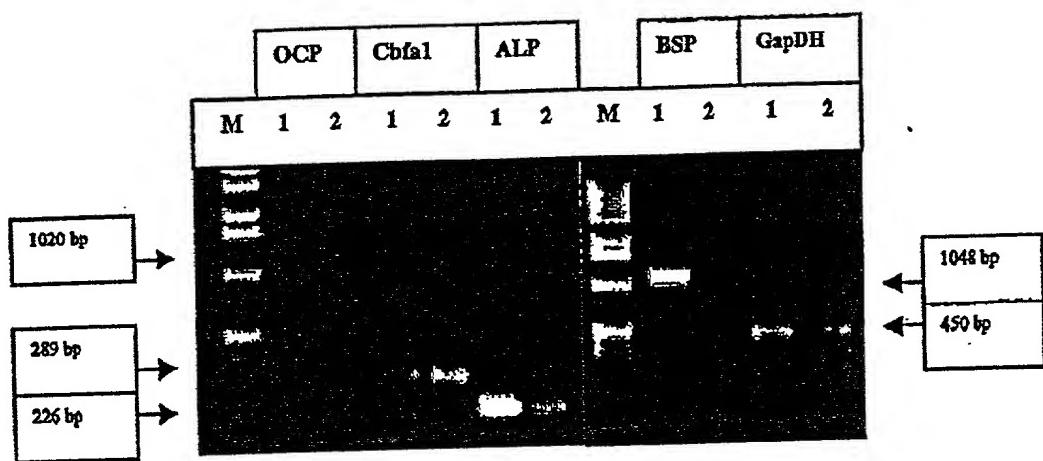


Figure 37

x4

x10

pCDNA  
ROS stable line

OCP  
ROS stable line

Figure 38

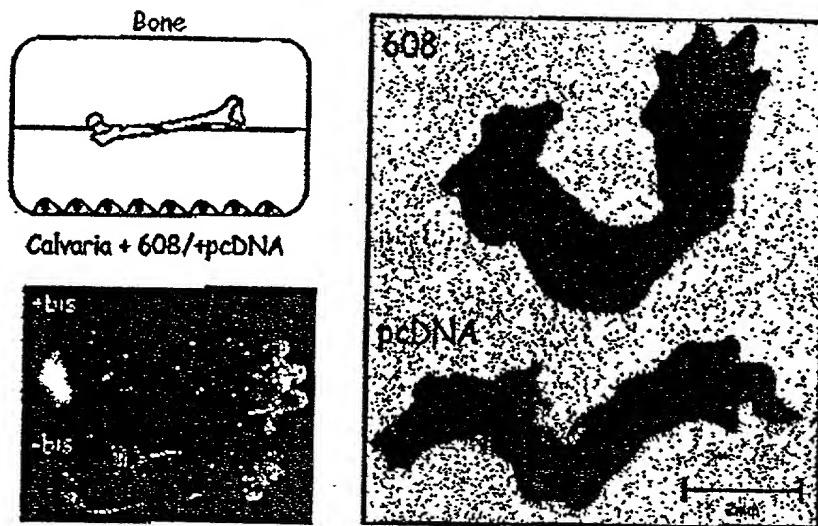
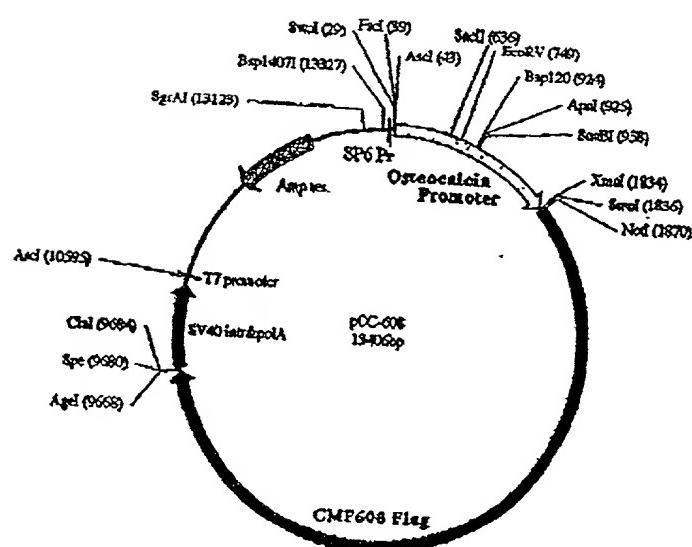
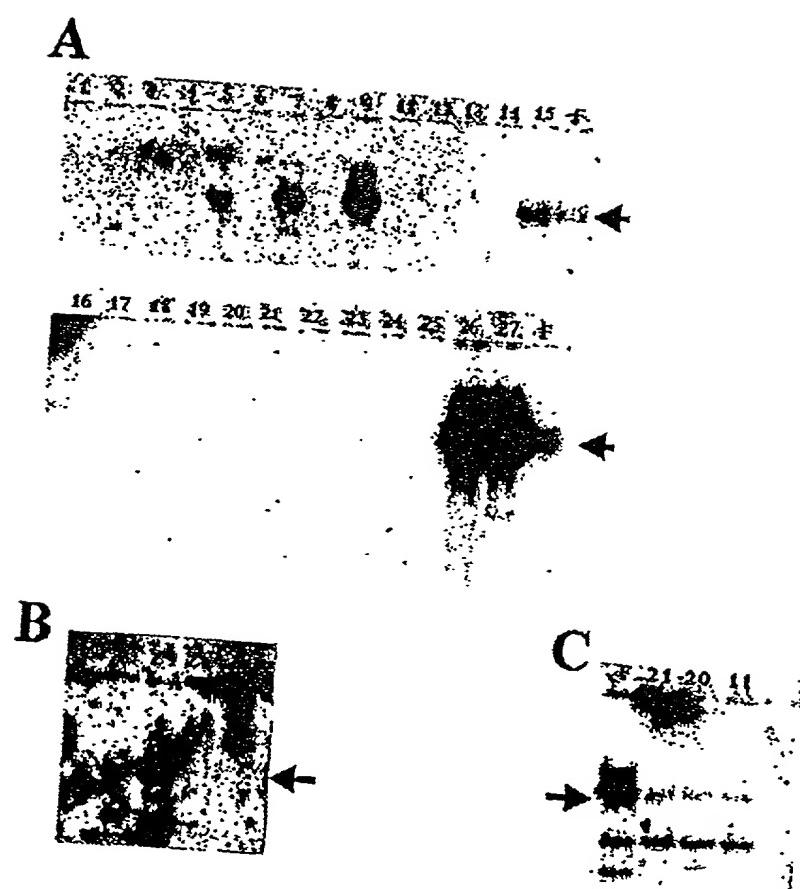


Figure 39



64/90

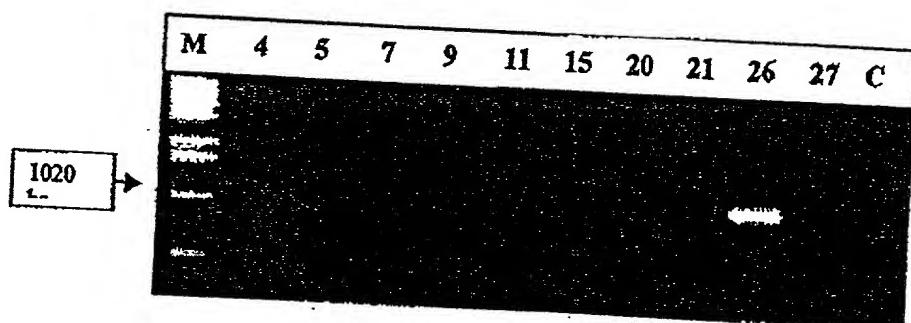
Figure 40



65/90

Figure 41

A



B

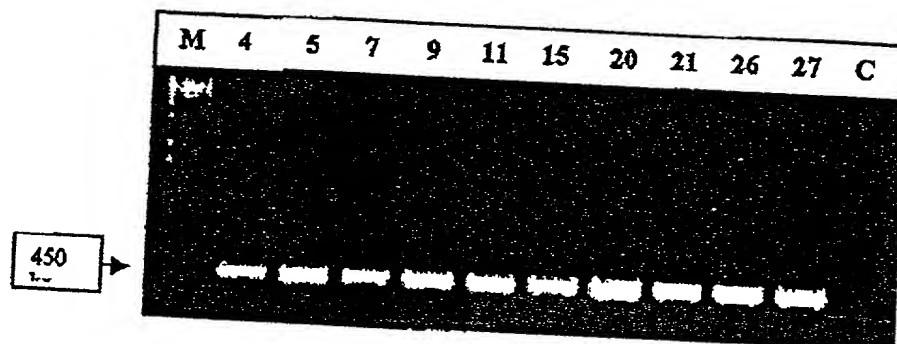
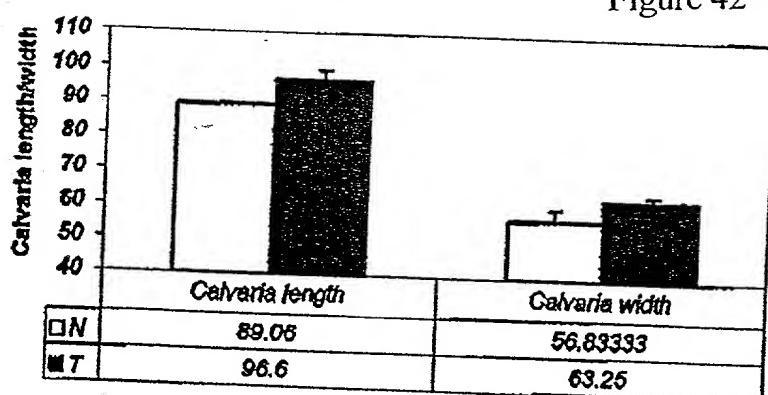
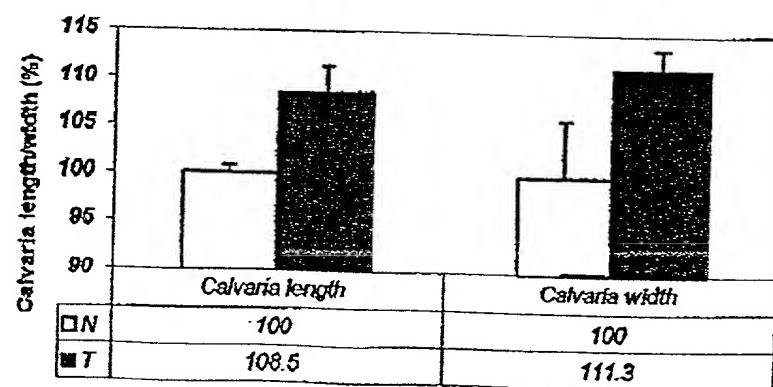


Figure 42

A



B



66/90

Figure 43

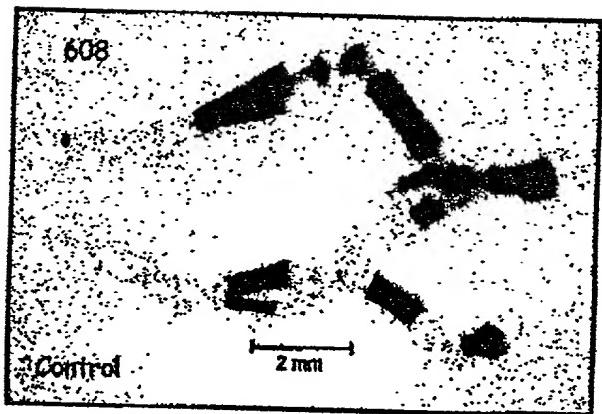
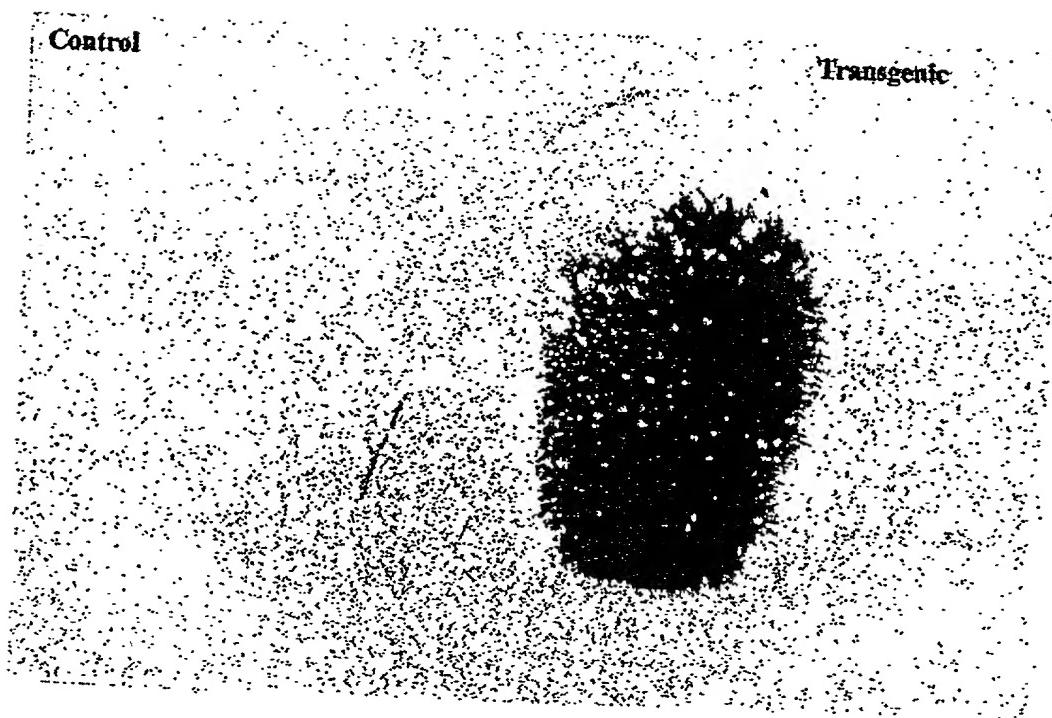
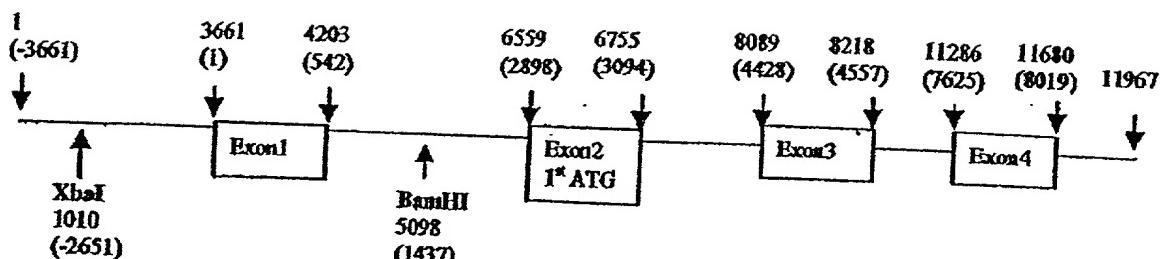


Figure 44



67/90

Figure 45



Clone 14C10 / 1SE11

← T7 orientation in pKS

Figure 46

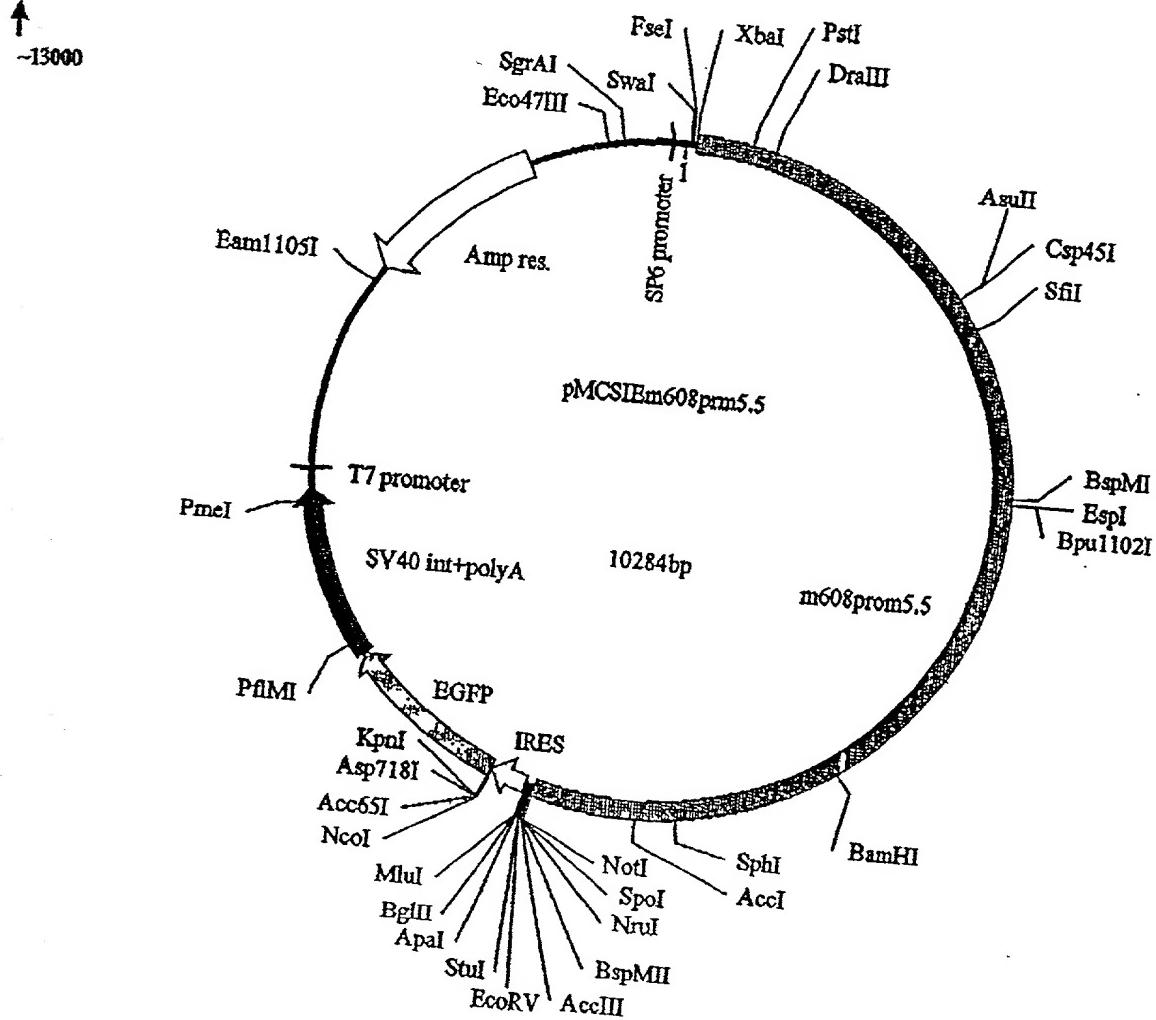


Figure 47

↓ (XbaI)

ICTAGAAGTAAAATGATCCGTAGTAGCGATCCGGAAAATACGTACTCTAACACACTGC  
AATCATCTCTCTGTGGTTGCTGGAGCTGAGGTCTGGAAAGGCTGACCTGGTTAGAAATA  
ACCTACCGAATACAGAGCTATGACGTTAGTCAGCTGGAGGAGCTTGGAAAGAAATGACAAGCT  
GTAGCTGCCAGAACATACTAGATGCCATATTCCAAGGCAAGTGTCCACATGCCGACAT  
CTTAAGAATATGGTTGCTCTGCAGTGCTAAGGACCTTGTCTGOCACACAGGTCTCCAG  
GGTTAGTGCTAACTCTGACTGCTGACTCTTAATTCTACCTGATCATTATGACTAGAA  
ATCACCTGGTGATTAGCAACTGGATATGGAATTAACTAATTGTACCCAGCCAGGCCAC  
CTCAGCTTGGAGCTCCATTCTGTGGAGCOAGTCACGTGGTTGAATCAACTGT  
ACTGTTCTACTTACAAGACGCATTACCTGAGATGAGTCATTCTCACAAGTCTTTTA  
GAAGAGTCATTAGACATATTCTGATGAGTAAGCATATAAAGTGAGAGCAGCATGAATG  
TGTTCCATGTATGCTCATGGATGCTATTATAATGGAATAAACTGACTTTAAAAAAA  
AGCTTATGATACTGTACAGAGTAAATCTCCATAAATATCATCTGCATTATAAATTAT  
TITCATAATCCATCAATTAAAAACCTTGTAGAAATTITGTTAACACAAAGATCCCTAGGCC  
CTGCCCTAGGATGTTGCTGTATGGTGGCTGAGGAGATGGAGCTTAAAGAACCTACTTGCTCC  
AGGAGCACATCTCAGAACATCTGCCCTAAACATTATGCCATTGCTCATCAAAGGCTC  
ACTCACATGTGCTICAACCACAGGGATTAAACAGTCATTGTACATTCTCAAACGGT  
GGAAGCCTGCTAGAGGAACAGGATGTACAGGATAACATCCAACCTACAAAAGGATGTC  
ATAACCCCTACCAACAAACAACACGACAACAAACCCATAAAAATTATCACGGCAAAT  
GAACTAAGCCATATGCAGAAAAAGTATTATATGTTCTCATGTTGGGTGTTTCTTAAAT  
AGTCAAATATGCAGAATTAGACAAAGATGGTTATGCAAGTGGGGATGGCGAAGGATA  
CTTGTAGATTAGAGGACACAAAGCAACAACTACAGAGTGAAGTAATCCAGAGACTTAATG  
TATAATATGAGGACTGTATTAAATAATTCTATTAAAGATAACAGCAAACGAGTGATCTT  
ACTAACACACACACTACATAGAGAGATAAAAGTGATAGATACTGTTGTTTATCTCTCATG  
TAGCTGATAATTCTATATTGTACACCTAAACATAGATAACCAACAAAGAGGAAGAGGAT  
AGGTGCTCTCCAGGGCGAAGAGTACATTGAAAGTCAGACACCATTGTGTAGATGTA  
CCACATGGAGGAGCTAGAGAAAGTAGCCAAGGAGCTAAAGGGATCTGCAACCCCTATAGG  
TGGAAACAACATTATGAGCTAACAGTACCCCGGAGCTCTGACTCTAGCTGCATATATATC  
AAAAGATGCTTAATGGCCATCACTGGAAAGAGAGGCCATTGGACTTGCAAACCTTAT  
ATGCCCTAGTACAGGGAAATACAGGGCCAAGGGGACTGGGTGGCGAGGGAGTG  
GGGGTGGGTGGATATGGGGACTTTGGTATAGCATTGGAAATGAAATGAGTTAAATAC  
CTAATAAAAATGGAAAAAAAAAAAAAAAGGAAGGTCAAGACACCTCAC  
TTCACTGCTATCTCAACTTGCAACAGAAGGGAGTCACAAACCCAGGACAAACACAGT  
GATTAAGCGCTTGAATGTTATTGCTGTGTTACCACTCATTAGCATATATTCAT  
TGTGAAAACCTACGGGTCTATGACATTTTATTCAAGTATATCACATGCTGTCAGC  
ATATTGGCACCACTACCAGCCCCAGCCCCCTTGGCCCOGCCCCAACACACACACACA  
CA  
CATCATCTGCTCACTCACCCACCCAAAGCTTAATCTTCTTCTGCAATAGTACCTCTC  
CTATTCTATGCTAGGTCCCCCTCCCCCTGTTAGGGAGATGGGAGGGTACGAAAGGAA  
AGAATTGTTAGCCCCCTGAGCCAGCCCCGGCCACAGAGGCTGCCACCAGACAGGAAAGCC  
CAGGGCTTACCAAGCAAGGAGGAGCAACTGCGAGGCGAGCTGGGTGGCGCTGGTGGT  
CCCAGGTGATGGCCCGGCCATTCCAGAAGCCGAGGCTATACTGCGTCACCTGCCCG  
CCCTCTCCGAGTGAAGACCCCTAGAGGCTGAGCAGACCCAAAGGCGGTGCAATTCCA  
TTGGCCCAAGGAGGAGGTGAGCGGTGCTTAATCCCTCGGAAAGTGAAGGGACCCAGAG  
Exon1  
AGCTGGTAGATGTGGGAGCTGGGGTCAGGGCGAGACAGAGGGTGGGATGGCGAGAAG  
GGTCCAGGAAAAGGAAAGTACTGGAGGGAGTTGGGACAAAAGCAGCCACCAAGGGAA  
CATGGCTTCACTGACTGAAAGCCAGGCAAAAGGAGGGAGGATTATATGTTAGGCTGGGA  
CGCTTCTATCAAACACTGATGACGTTGCTAACAGCAAGCAATTGAGGAGAAACGCT  
GGGACGTCGGAAAGAAGGAGTGAATGATTAGTACTGTAAGTTAGGTGAGTTGAGAAC  
TAACAACTTATACTATTGAGGGAGAAGGAAGGAGTACCTCAAGCAGCAGCAGCAGCA  
GCAATCAGATAAAAGGAAAGCTTGGTAGTTGGAAATGTTGATGACCAATTAAACA  
GAAGCGCTTCACTGTAAGAGTCAGTCCCCCAGCTAGTGAAGACTAAGCTACTAA  
GCCTTTGCTCCGTTGAAAGCAAGAACGTTCTCAATCAGGTGAGGCTCTCAGA

AGATTTCTGTCCTGCTTACAGAGGATTCAAAGCAAGACAGAAGAGCTCAGG  
 TATTGCCAACTCTTGTAAATACAGTTGAGGCTTAAGTGTACGGGAACCTCATGTGTTA  
 TTCACTTACGGCTCTCTCTTATAACTAACTCTTAAGGTGCATATAGTCCTCTGTTCC  
 CAGCTACCTTGACATCTTGTATCTAATAATAGCAAGCTCATCTGCTTTAATCATC  
 ACGCAGAGAGTATTCAAAAATATTCACTGATGTAACAGTGCAGCTGTAGGCATAGAAGTA  
 ATCATTAGTAAATCTTAAATTGGGTTAAACTCATTCTAACAGCTCCAGGTGGGAGGGAT  
 CACTGAGCCTCGCCAOGTGCGGGTTAAAGATATTCTAACAAAGAGAACAGCAGAATTCTC  
 CTGGCCATGCTCCCCATCACTGTGTCAGTAAGCAGAGGGGTGTTCCAAGCAGAGAAAG  
 AGCAGACAGTGTATGCCCTGCAAAGTCAGAGACTCAGCCCTCCAGCTGGTCAGTTACT  
 GTCTCCCGTCATTAGTGGCTCTGAAAAGGCCATGTGCTTATTGGCAAGGACTTGC  
 AGACATGCTAGAAAGAAATTGACCTTTCTAGGGTIAATTACAGCTGTAAGAAGTAT  
 TTGGAAGGITAAGCAAATAAAACACATATTAAATAATACAATGTTACAAAAAATT  
 GATCATATAAAGAAGTACATTCAAAATGCAATGTGAAAAATATATATAATTATCTAT  
 TTACTGGTGCAAAGTTCTAAATTGCACATGTACTATTITATATTATAAAAATATTIT  
 AAAATGTATATAAAAGTGTAAAGGCTTGGTCAAACAAGAGAGTAAATTACAAACT  
 ↓ (BamHI)

TTAATTGCCCCATAACATTATTATGATCTCAATGACAGGGATCTGCTTTCAATTGGGA  
 AATGAGAAGCTATGAGATATGTTACATAATAAGCCCATTAGTGTATAAGTCCAATG  
 GGAAGCTAGCACACACTGGTTATAAAGAGAACAGTTCTGAGTCTATGCAAGTTACA  
 CTCTAGGGATAAGAGTCCCTCTTCTCCAGATTTCACTAGCATTGTTGTCATCAATTATC  
 TTCTGATGATGAGCATTATAAGTGGATAAGATAGGATCTCAAAGGAATGTCATTGG  
 ATGCCCTGAAACAATTCTCAGGCTTCTCAGTTCACTAGTCTATTCAATTATTGGATAA  
 TTGGGGATGGTGTAAATTITGCACTTCTATGGAATTCCAAAAAACAAAAAACAAAC  
 AAACAAACAAAAAAACCTCTGAAACTAGAACACTACCAATTCTACTGGGTATGTAACAAAG  
 AGAAAATGCGACAGAAATTATTGCTACATTGTCATTATTCAGGACAGCCAAGAATGTGGA  
 ACCAACCTACGTAGCCGTAAAAAGAGTGAACGGATAAGAAAATGTGGAATGTCACAAAC  
 AGAGTCCCCTGTTGGCATAAAAGAGTGAACATGACATATGCAAGGAAATGGTGTAGCAACT  
 GGAAATCAATTGGGTAATCAAACAAAGACAGACTCAAAGGGAAACCCGTGTAGCCT  
 CTCTGACAAACAGAAGCTAGATTACACTTGTACGTGCGCATGTGTTAGAATTATT  
 TAGTTATACACTATTCTAATCTGAGTGTGTATAAAGGCATGCTGTAAAGCAAGC  
 AGCTAGCTGGGTGGTAGGAGAGAAAGCAATGAGAGGGAGTTAAAGAACAGACAGATA  
 GTAACATAGGTGCCAGGATGAAATGCAATTATTGTATGCTAACTAAACCACAGACAGGA  
 GGCACAGCTCAAACCCAGGGTGAATCCAGCACAGAGAAGGGAAAGTAGACACAAAGT  
 TTGCGCACTAACCAAGAACGCCATTGCACTTGTGCTGCTGGGAGGGCGTCCAGTTT  
 CTCCAGTGTGACACTGTTATAACAAACCGATTGACAATACAAGTTGGCATGATGGATGG  
 TTTTGTGCTATTCTCATTCTTCTTACTGTTGTGTGTTGGGGTGTGTTGGTGTG  
 GCTGTGGTTTCTATTGTTCTTGTGAGAGAGAGAAGGAACATGAAATTGGGGGGTAGGA  
 AGCTGGAAACGATCTGGAAAGAAGTGGGAAAGAGAAAAATTGTATGGAGCATATTAA  
 ACAAAACAAACAAACAAACAAAAGGTCTATTGCGCACAAAAAGGTGTGAATTAAATTAAAC  
 CAGTTACGACTCTTAAAGAAAATATTCCCAATTATTCCAGAGTTGCTATGATGCTGTC  
 CTAGGACTTTGCTGAACTGGCCCTATAACTCTGGTGTGGTGTCTTCAAGG – Artificial

Notizie

(SEQ ID NO:17)

Figure 48

CACAGACCTTCCCTCTAACCTCTCCTCCCCATCTTGTGCTTCATCCAGACTTCACAC  
 CAGCAAGCACACTCGTAATGCAAGGGCTGCTCTGTCAGGACAACAAGQAGGCTGAAG  
 GCAGACCCACACGTTCCAACGTGCTCTGAGAGTCATCCCTAGACTCATCTATAAGCAG  
 GAAACCTGCTGTGATCTCCATTCTCTGACCACATCCCCAAGTTATCACAAGGAGTT  
 TTCTCTCAAAACCTTCTCTCCAGCAAACCCCTCACTGCTCTGGGTACTTTCTAGCCCC  
 TCATGGGAAACCTGTGCTCCATCCAATGGATGGCTGTGAGCATCCACTCTGTATAGAAT  
 CTGGTCAGTGCACTCTTGTATCTCAAGAACACTGGGCTGAAAATTAAACCCAAAG  
 AACTGTTTTTGTTATGATTTGCTGCACTCTTCAATTCCAATAAGAGTAAGCATCTCAT  
 TCCCTGTCTCCCTTCAGTACCACTGCCTTGTGCTGCCCTCTCAAAGAATCAATAAA  
 ACCAAAGTGTATAGATTCACTGGCACTCTCTAACTGCTACATCCACTCCAGTAGTATCTC  
 ACTTGGCAGGTGAAAAGCTGGAAGCAGTCACGAGGAGTTACAGAAACTAGCCTC  
 CTGGAAACCTTGGCATTCCCATAGCTAGAATGCCAGATTGTCCCTGAGATATTGTGGTG  
 GGTCTGCACTGCTTCTGCACTTACTGGATAAGAGTTAGAAATCTCAGGGCAGCT  
 TAGCAAAAGTATACTAGAATCTCATGACAGTCAGGTATTGCAAACACTACATTGCAATT  
 GAAGAAAGTGGTAAATTCTCTGACAAATGGAGATTCCCTACAGATAACTAAAGAAC  
 AGCTAAGTCACACTCATATGCAAGAATTACCAAGGCTAGGAAAGGGGGGGGGTACT  
 GCTTATTCTCATGATAAGGTCTGCTAGAGCAGAACCCCTGGCTGCTACTTCACAAGGTC  
 AAAGGTGTAGCATAAAATTGTGACTAGAGTGTGAAATCTTACCTGTGATTAGCTGACTCTA  
 GGCAGAGCTTCTTACTCTTACTGTAAACATTACCTGGTCTGTGACCTCCCTTGAAGGCAT  
 TCCCTGTCTTGTGACAGATACTCTATGTAACCTGGCTTGTGACACCCCTACTCCCTTGT  
 TTCTGTATTATATAAGCTGGTGTCCCTTGTGAAAAAATTACATCCAGATAACGCACTC  
 CCTTGTGTCTGTGCTTGTGCTATTCTGGCCAACCTCATGCCACCTGCCAGAACCCCTA  
 GTCTTCTCACAGATTGGGGAGGCGACTGAGCTGGCTGGTCCATGGCATCTAACCACTGTCA  
 GCTCACTGTGGTACTACCTCAAGGTACAAGCTCCATTACTAATGAAACAAAATTAGAT  
 AAGTGTGGTCCAGGAAGCAGGGTGTACACCCCTGTGAAATGAAACATTATGAAATGACTG  
 AAATAAGTTAACCCATCTCTCTGTTGCTAATATAGCAAATAACCGAGTTCTGAGC  
 TGCTGCTGGTGTCTCATGAGGGCAGAGCCAGTCGATCTAGCTTCTGTATGTG  
 TGTCCATTGTTCTCAGTCTCTGGTGTGCCCCATTAGGAAATCTAAGCCATGAAAGCCATG  
 AATCTGGGAATGACTTTCTAAGAAATGCCACGTGAACCTTGTGTTCAACGTTTGCCTG  
 TAAACAGATATATGGTGCCTGAGTTATAATCATAATAAGCTTGTGAAATAATATAACCT  
 CATTCTCATCTGCTTCCACCGTGGAGCTGAGCTCCCTGGGAGGACCAAAAGGCAATTG  
 AAAGTAGTGTATTATGACCTGCTTGTGTTACTAATAAAAGCTCATGAAAGGGCAGCC  
 ATGTTGAAACATGGAACATTGGGGTGCACGTGATCTGTTCTGGGTGCTGACTCATA  
 TTGTCCTCAGAATAAATGAGTTATCAACTCTGAGGAAAAGTTGTGTTGTATAGCA  
 CGCCCGTGGAGTOCCACCATCTACTCTCTGTAATCTGTTATGGTAGAAAAGTTAATT  
 ATGTGATTCTCCAACCTCAAATATTCTAAATCTTCTGCTGCTGGGATTCTTGT  
 ACTAAGTCTATGTTGAAAGATCTGAGCTGGTIAAGGATTGCACTGATGTTACAG  
 TCAGGCTAAGCTGAAAAATGACAAATGAAATGCAATGTCATGTGCCCTGGGATGTG  
 AGTGTAGGGGTTAAAGAAACAAATACCTACTCTAAATAGTTAATAAGTCCCCTGGGTT  
 CTATCTAGTTGAAATAATGTTCTCTAGTATACTACAGCAATTAAITGAAATGAAATGCTC  
 TTATCTGACCAATCTCAGTGCATCTCATCCGCTCCAAAGTCATGTTCTCATATTCTACAAAGGAT  
 AGGTCTCATTCAACCACATGTTATCATGGATCTGCACTTCTGATGCAAATGATT  
 ATTCTCCAGAGCACTGAAATTGGGTGAATCATCTTATAACGCCAAAACCTAAATGCTC  
 TGTGCTAAACAGAGAGTTACAAGACCTTTATGTTGATGGCAGCATTAGTCATCCCTA  
 TGACAGAAATGTCAGGTGGAGCTCCACTGGGGAGGGCTGGCTCTGGCAGGATCTC  
 TTGGAACATCACACAAAGAAATTCAAATTATGAAATGCACTGATCCATCCAGAATGIG  
 ACTTTGACTCTGAAACATGAGCTTTAAAGTACGTTGGCTGTCAGACCTTGACTTGTG  
 GTGAAGGAAAGCTGCCAACACTCTTTTATGTAACACAATATCAAGATCTAATGIG  
 GACAGTATGCCAGTCCCAGAGTCATGTCATGAAAGACACATTGCGATGTTACACT  
 AAGGAGGAGAAGGCAAGCTACAGTGAAGCCAGTTCACTATAAGCTTATGAGAAATT  
 AGATAAGAAGGGTTCTAATTAAATTTTTATTAGATAATTCTCTCATTTACATT  
 AAATGCTATCCAAAAGTCCCCTATACCTCCCCCTCACCTGCTCCCCCTACCCACCCACTC  
 CCATTCTGGCCTGGTTACTGTGATAGTGGCTCATATGATCACCAGCCTTACATGCTC  
 ACTATCTGGCTATTGCAAGAATGGCTGCGAGCTGATGCACTGAGATAACAGACACCTAC  
 AGCCAAACAGTGGAAAGGAACCTGGGACTCTATGGAAGAAAAGGAGGAAGGGTTATGG

GCCTCGGATGGGGAAAGGAACCTCACAGGAAGACCAACATACTTGGTCAACTAACCTGG  
ACCCCTGGGCTCTCAGAGTCAGAACCAACCACCATAGAACATTCACTGGCTGTACCCAG  
GCCTCTOCACTCATATGTAACAGATATGTGGCTTGGCCTTCATCTGGTCCCTGAACAACTA  
GATGGGGGTAGGGGTGGGGATGGGGITATCTCAAAAGCTGTGCGCTGTATGTGGGATA  
TGTTCTTACTGAGCTGCCTAGTCTGGCTCAGTGGAGAGGAAGCACCTAGCTTAGCCTT  
GTAAAGACTGAACTCTGAGGTGTCGGTGGAGGTATACTCAGGGAGGGCCTCACCTGC  
TAGGAAGAGAAGAGGGGGGGAGACTTGAGGGAGGGGGCAGTGAGCAGGTTGGTAAA  
ATGAATAAGAaaaaaaaaaaaaATAATTaaaaaaaaaaaaAGAATGGCTGCTGAGCCC  
TACTCTAAAACCATTCGATCCCCCCCCCCCCAATCATTCACTGACTACGAATTAAATCATT  
GATACTAACATAAGATGTAGGAAACTATGTTACTCTTGTGAACTACAGGTGGTATTTG  
GAACCTTTTATTGAAGCTTTCACACAGGCCCTGTTCTTCATTCCCTGTACATGCATG  
TAGCTTAATGATGTTCACTGAATTAAAAATAACAATGAAGAATAAGACAACTGTATTTT  
AAGGATTCTCGTATATATTTAAAAATCTAAGGTGGTCACCTGGAGAAAATGTCITCAGTT  
TTTCTATATAATGTTACTCTATOGTATGTTAATTAAATTATATGCAATAATTCAATAAACTA  
CAACATAGTATGTAACCTATAAGAAAGTAAAACATTCACTGAAATTGTGAAGGTACTTTTC  
CTTACCTCAGAAACACTGGGTTTGAATAATTCTTATTGTTATCAGTGAAAGAATTGAA  
AGAATGTAATAACCTACTAAGGCAAACATAGAAGGTGAAATTAAAAAGAGTAGACAGGA  
GAAGTAATAAGGCAAATAATGAATATTGCTTAAATAGTTCTTAATGTTATCATTCAACTA  
GGGTGTGATTCTCCAGACTTGACTCCATCCAAAATGACTCTAACCAACAGTCA  
TTGAAACAAATGTGTTGAAAATAATAAACATTCTCCTACTTGAAAATTCAAGATTCTCCTACT  
TTGCTTTTATTGCTGTGATAAGCACCAGACCAAAAGCAGCTTAT

(SEQ ID NO:18)

72/90

Figure 49

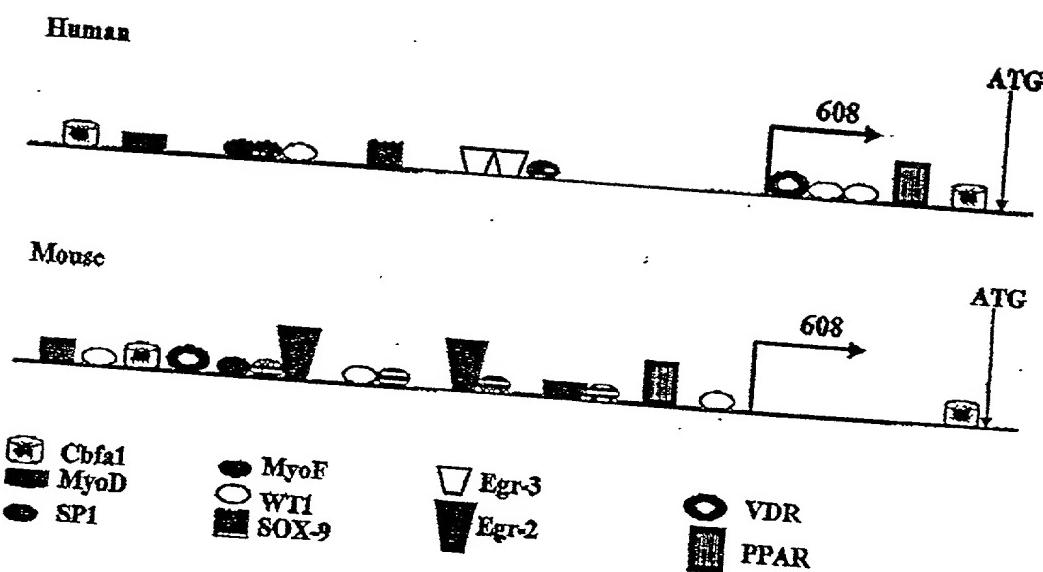


Figure 50

TAAGCCTTGTCCC GTT GGAAGCAAAAGAACGTTCTCAATCAGGTGAAGGCTCT  
 CCTCAGAAGATT CATGTCTCAGCTTATGTTACAAGAGGATTCAAAGCAAGACAGA  
 AGAGCTCAGGTATAGCCA ACTCTTTGTTAAATACAGTATGAGGCCTAAGTGTACGG  
 CAACTCATGTGGTATT CATTTGCGGCTCTCTCTATAACTAACTCTTAAGGTGCA  
 TATAGTCTCTCTGTTCCAGCTACCTGCACCATCTTGTTATCTAATAATAGCA  
 AGCTCATCTGCTTTAATCATCACGCAGAGAGTATTCAA AAAATTCACTGATGTA  
 ACAGTGACAGTGTAGGCATAGAAGTAATCATTAGTAAATCTTAATATGGGTAAACT  
 CATTATAACAGCTCCAGGTTGG (SEQ ID NO:19)

TTTGGAACCAACCCAGATGCCCTCAACAGAGAAATGGGCCAGAAAATGTGGTCCA  
 TTTATCCAATGGAATACTACTCAACTTATTA AAAACACGACTTTCTATAAAATTTTA  
 GGCAAATGNATGGTCTGNAGGATCTGAGTGAGGTAAACCAATCACAAAAGAACAC  
 TCATGGTATGCACTCACTGATAAGTGGCTATTGTCATGGAGTGATTAAAAGGG  
 AGAAGACACATAGCTTTGTGTGTATAATATTAAGATGGAAATTGCCAGTGCTGT  
 TTGGCTTATGAGTGAATCTGTTCACTGGATTACCGGAAGAAAATAATAAGTGAAC  
 TGTAGGAAGAAGTAGTTAATCAAGGTGACAAAGTATCCTGACACATTGGGAAAAGA  
 CCACAGTCCAGGAAACTGAGTCTTAAGGATTATTAACCTCCAGTTCCCCATGTGC  
 AGCTCTGAGACTTGGCAGATCAGACACTTAACCTACCAAGCTTCCACACAGAGCA  
 GTTACTATCCTGCCTCACACATGGAGTGTGCCATTAAGTGCCTGAACATGAGTCT  
 GACTTGTAAATAATCTTAAAATCCAATTGTGTGTAAAGTATGTGACCAAAGAGCAT  
 GGTCTGCTATTAAACCTTGTGTTCTATGGACTCTTAATTGTAGAAATGTCA  
 ACAAGCTTGTGGAGGCTGGAAGATAACAGGCTTAAGAGGATGGCCTTCAGTTG  
 AAAGTAATTCACTATGTGTTCTGGCATCCCTTCTAAAGCAATTAAACCCCCAA  
 GTAGGCATAATTAAATGCTTACTTCATCAGAATATATCTAATTGACTCTCTAAAAA  
 GACTTGGTATGCATAGGATCTAAATGTAATGTGATTACTGACATAATAAATAGG  
 AGAAAATGAGCTAGAATAGGTATAAAATATGTGCTGGCTTCTAATAGGTCTTATAG  
 GITATATAAGAGGGGGAAAGGAATATTGAAACATCTAGAAGTAAATGATCCTG  
 AGTAGCGATCCTGGAAAATACGTACTCTAACACACTGCAATCATCTCTGTGGTT  
 TGCTGGAGCTGAGGTCTGGAAGGCTGACCTGGTTAGAAATAACCTACCGAACATAC  
 AGAGCTATGACGTTAGTCTGGAAGGAGCTTGGAGAAGATGACAAGCTGTAGCTGCC  
 CAGAACATACTAGATGCCATATTCCAAGGCAAGTGTCCACATGCGGACATCTTAAG  
 AATATGGTTGTCTGCACTGCTAAGGACCTTGTGTCGACACACAGGTCTCCAGGG  
 TTAGTGCTAACTCTGACTGCTGACTCTTAATTCTCCCTGATCATTAAATGACTAGA  
 AATCACTTGGTATTAGCAACTGGATATGGAATATTACTTAATTGTACCCAAGCCA  
 GGCCACCTCAGCTTGGCAGCTCCATTCTGTGGAGGCCAGTCACGTGGGTTG  
 AATCAACTGTACTGTTCTACTTACAAGACGCATTACCTGAGATGAGTCATTCTTCTT  
 CACAAGCTTTAGAAGAGTCAATTAGACATATTCTGATGAAGTAAGCATATAAAG

TGAGAGCAGCATGAATGTGTCATGTATGCTCATGGATGCTATTATAATGTGGAAA  
 TAAACTGACTTAAAAAAAGCTTATGATACTTGTACAGAGTAATCTCCATA  
 AATATCATCTGCATTATAAATTATTTCATAATCCATCAATTAAAAACCTTAGAAA  
 TTTGTTAACACAAAGATCCCTAGGCCCTAGGATGGTCTGTATGGTGGGCC  
 TGAGAGATGGAGCTTAAGAACTTACTTGCTCCAGGAGCACATCTCAGAACATCTGC  
 CTCAAAACATTATCCAAATGCTCATCAAAGGCTCACTCACATGTGCTCAACCAC  
 AGGGATTAACACAGTCATTTAGTCACATTCTCAAACGGTGGAACGCTGCTAGAGGA  
 ACAGGATGTATCAGGATAACATCCAACCTTACAAAAGGATGTCTAACCCCTACCA  
 CAACAAACAACGACAACAAACCCATAAAAATTATCACGGCAAATGAACTAAGC  
 CATATGCAGAAAAAGTATTATATGTTCTCATGTGGGGTGTCCCCCTTAATAGTCAA  
 ATATGCAGAATATAGACAAAGATGGTTATGCAAGTGGGGATGGCGAAGGATACTT  
 GTAGATTAGAGGACACAAAGCAACAACACTACAGAGTGAAGTAATCCAGAGACTAAT  
 GTATAATATGAGGACTGTATTATAATAATTCTATTAAAGATAACAGCAAACGAGTGT  
 ATCTTACTAACACACACACTACATAGAGAGATAAAAGTGTAGATACTGTTGTTT  
 ATCTTCATGTAGCTGATAATTCTATTGTACACCTCAAACATAGATAACCAACAAA  
 GAGGAAGAGGATAGGTGCCTCTCCAGGGCGGAAGAGTACATTGAAAGTCAGACA  
 CCATTGTGTAGATGTACCACATGGAGGAGCTAGAGAAAGTAGCCAAGGAGCTAAAG  
 GGATCTGCAACCCCTATAGGTGGAACAACATTATGAGCTAACAGTACCCCGGAGCT  
 CTTGACTCTAGCTGCATATATATCAAAGATGGCTAATCGGCCATCACTGGAAAGA  
 GAGGCCATTGGACTTGCAAACCTTATATGCCCACTACAGGGGAATACCAAGGCCA  
 AAAAGGGGGAGTGGTGGCAGGGAGTGGGGTGGGATATGGGGACTTTT  
 GGTATAGCATTGAAATGTAATGAGTTAAATACCTAATAAAAAATGGAAAAAAA  
 AAAAAAAAAAAAAAGGAAGGTCAAGCACACCTCACTCACTGCTATCTCAACTTG  
 CAAACAGAAGGGAGTCACAAACCCAGGACAAACCAACAGTGATTGAAGCGTCTTG  
 AATGTTATTGCTGTTGTTACCAACATCATTAGCATATATTCTATTGTGAAAACCTA  
 CGGGGTCTATGACATGTTTTTATTCAAGTATATCACATGCTGTCAGCATATTGGC  
 ACCACTACCAGCCCCAGCCCCCTTGCCCCGCCAACACACACACACACACACAC  
 AC  
 TCATCTGCTCACTCACCCACCCAAAGCTTAATCCTTTCTCCCTGCAATAGTACCTC  
 TCCTATTATTGCTAGGTTCCCCCTCCCCCTGTTAGGAGATGGGAGAGGTACGA  
 AAGAAAGGAATTGTAAGCCCTGAGCCAGCCCAGGGCCACAGAGCCTGCCACAGAC  
 AGGAAAAGCCCAGGGCTTACCAAGCAGAGGAGGAGCAAACCTCGCAGGCGAGCCTGG  
 GTTGGCGCTGGTGGTCCCAGGGCTGATGGCCGCCATTCCCAGAACGCCAGGGCTATA  
 GCTGCGTCACCTGCCCTCCTCCGAGTGAAGACCCCTAGAGGCTGAGCAGAC  
 CCCAAAGGCGGTGCAATTCCATTGGCCCAAGGCAGAGGTGAGCCTGCTAATCCC  
 CTCGGGAAGTGAAGGGACCCAGAGAGTCTGGTAGATGTGGGAGCTGGGGTCAAGGG  
 CGAGACAGAGGGTGGGATGGGCAGAAGGGTCCAGGAAAGGAAAGTACTGGAGGG  
 AGTTGGGACAAAGCAGCAGCAAGGGAACATCGCTTCAGTACTGAAGCCAGGCA  
 AAAGGAGCGGGAAAGGATTATATGTAAGCCTGGACGCTTCATAAACACTGATGACG  
 TGTTGTGCAAAGCAAGCAATTGAGGAGAAACGCCCTGGACGTCGGAAAGAAGGA

GTGATCGATTAGTACTTGTAAAGTTAGGTGAGTTGAGAACTAACA  
 TTGAGGGAGAAGGAAGAGCATTCCAGCAGCAGCAGCAGCAATCAGATAA  
 AGGAAAGCTTGGTAGTTGGAAATGTATGATACCATTAAAATAACAGAAGCGCCT  
 CCAGTTCTCTGAAGAGTCAGTCCCCAGCTAGTGAAGACTAACGCCTACTAACGCCTT  
 TGCTCCCCTTGGAAAGCAAAGAACGTTCTCAATCAGGTGAAGGCTCTCCTCAGAAG  
 ATTCCTGTCTGCTTATGTTACAAGAGGATTCAAAGCAAGACAGAAGAGCTCAG  
 GTATTGCCAACTCTTGTAAATACAGTTGAGGCTTAAGTGTACGGAACTCATG  
 TGGTATTCACTTACGGCTCTCTCTTATAACTAACCTAACGTTGCATATAGTCTC  
 TTCTGTTCCCAGCTACCTGTACCATCTTGTATCTAATAATAGCAAGCTCATCT  
 GCTTTAAATCATCACGCAGAGAGTATTCAAAAATATTCACTGATGTAACAGTGACA  
 GTGTAGGCATAGAAGTAATCATTAGTAAATCTAATTGGTTAAACTCATTCAA  
 CAGCTCCAGGTTGGGAGGGATCACTGAGCCTCGCCACGTGCGGGTTAAAGATATT  
 TCTAACAAAGAGAAGCAGAATTCTCCTGGCCATGCTCCCCATCACTGTGTCAGTAA  
 GCAGAGGGGTGTTCCAAGCAGAGAAAGAGCAGACAGTGTATGCCTGCAAAGTCA  
 GAGACTCAGCCCTCCCAGCTGGTCAGTTACTGTCCTCCGGTCATTAGTGGCTCTG  
 AAAAGGCCATGTGCTTATTGCAAGGACTTGCAAGACATGCTAGAAAGAAATT  
 GACCTTTCTAGTGGTTATTACAGCTGTAAAAGTATTGGAAGGTTAGCCA  
 AATAAAATAAAACACATATTAAATAATACAATGTTACAAAATTGATCATATAAAGA  
 AGTACATTCAAATGCAATGTAAAAATATATAATTCTATTACTGGTGC  
 AAAGTTCTAAATTGCACATGTACTATTCTATTATAAAAATATTAAAATG  
 TATATAAAAGTGTAAAAGGCTTGGTCAAACAAGAGAGTAAATTACAAACTITA  
 ATTGTCCCCATAACATTATTATGATCTCTAAATGACAGGGATCTGCTTCAATTGGGA  
 AATGAGAAGCTATGAAGATATGTTACAATAATAAGCCCATTAGTGTAAAGTCCA  
 ATGGGAAGCTAGCACACACTGGTTATAAAGAGAACAGTTCCCTGAGTCTATGCAA  
 GTTACACTCTAGGAATAAGAGTTCCCTTCTCCAGATTCACTAGCATTGTTGT  
 CATCATTATCTTGTGATGAGCATTATAAGGAAATAAGATAGGATCTCAAAG  
 GAATGTCAATTGGATGCCCTGAACAATCTTCAGGTCTTCTTCAGTTCACTAGTC  
 TATTCAATTATTGATAATTGGGGGATGGTGTAAATTGTCAGTTCTATGGAA  
 TTCCAAAAAAACAAAAACAAACCAACCAACCAACCAACCTCTGAAACTAGAAACTACC  
 AATCCATTACTGGGTATGTAACAAAGAGAAATCTGCACAGAACATTATTGCTACATTG  
 TTCATTATTACGACAGCCAAGAATGTGGAACCAACTTACGTAGCCGTCAAATATG  
 AACGGATAAAAGAAAATGTGGAATGTGTACAACAGAGTCCCAGTGGCCATAAAAG  
 AGTAAATCATGACATATGCAGGAAATGGATGCAACTGGAAATCAATTGGCTAAT  
 CAAAACAAGACAGACTAAAAAGGAAACACCGTGTAGCTTCTGACAAACAGAAG  
 CTAGATTACACTGTACGTGCGCATGTGTGTTAGAATTATTAGTTACACTA  
 TTCTAATCTGTGAGTGTGTATAAAGGCATGCATGTAAAGCAAACAAAGCTAGCTG  
 GGGTGGGTAGGAGAGAAAGCAATGAGAGGAGTTAATAAGAACGAAGCATAGTAAC  
 ATAGGTGCCAGGATGAAATGCATTAATTGTATGCTAACTAAACCACAGACAGGAG  
 GCACACGTTCAAACCAAGGGTGAATCCCAGCACAGAGAACGGGAAGTAGACACAA  
 AGTTGCCACTAACCAAGAACCCATTGCAAGTTGCTGCCTGCTGGGAAGGGCGTT

CCAGTTCTCCAGTCTGACACTGTGTATAACAACCAGTGACAATACAAAGTTGGC  
ATGATGGATGGTTTGCTATTTCATTCTTACTGTTGTTGTGTGGT  
GGTTGTTGTGGTGGCTGTGGTTCTATTGTTCTTGAGAGAGAGAAGGAAC  
ATGAAATTGGGTGGGTAGGAAGCTGGAACGATCTGGAAGAAGTGGGGAAAGAG  
AAAAATTGTATGGAGCATATTAAACAAACAAACAAACAAAAGGTCATT  
GCCACAAAAAGGTGTGAATTAAATTACCAGTACGACTCTAAAGAAAATATTCCC  
AATTATTCCCAGAGTTGCTATGTATGCTGTGCCTAGGACTTGCTGAACGGCCCTA  
TAACCTGGTGTGGTCTTCAGGATGCAGAAGAGAGGCAGGGAAAGTCAGCTGCT  
TGCTGATCTCCCTCACTGCCATCTGCCGGTCAACCGGGAGCAGGGTCTGTC  
CTCGCCGATGTGCCTGCTATGTGCCACAGAGGTGCACTGTACATTGGGACCTGA  
CCTCCATCCCAGACGGGCATCCCAGCCAATGTGGAACGAGTCAATTAGGGTGTG  
GACCTTGCCGTATCTCCTCTCAGAGAGGGACACTGATTTCCTGGTACTTGCCCC  
CCAAACACCTGTGATTACTTTAATAGTTCTCTAAATGGGTCATACAAACCTT  
ATATTGTGGAGACAATGAACATTATCCAATAGTCTTACTAGAACTTGAAGCC  
CCTCTTAGTTGTTGGGAGCCTCATAATTATGGGCAGCTTATTCTGAATGAATT  
AAATGAAAAAGATACTGTTCTGTTAACAACTCATATTGATACCAAGGAAGAGGAAT  
TGTCAATTGAATATTAAAAAGCATTTCTTGCATTGCAATTATAAATACCCATTACAA  
ATGGCTTACTTAAATACTTGCCCTACTAAATCTGACAAATTATGGTGTATTGAA  
GGTTATGAAAATTGTTATGTGTATAAATGCACAAGAAATGGGATATGCCATCAC  
CTATGTGCCATTAGTGAGCATGTACAGTATGCCAAACACTATTGTCACGTTGGAG  
GAAGTAATGGGGTGGGGAGCAACAAGGGTATAACCGTATACCCAGTGCCTTGG  
AAGCGATTGCAAACAGTAAAGACTGACATTGTTCTCCCTATGAGGGAGGGCCTT  
GGGCTGAGCACTTGCAATGAGCATTGCTATTGCTGGCAGGTTTATGATAAC  
TTGACCCAAGCTAGAGTCAGGAGAGGAAGGAACCTCAACTGAGAACATGCCTGA  
AGAAGATCAGATTAGGCAGGCTGTGGGCATTCTTAATTAGTGATTGATGG  
GCAGGGCCCAGTCCATTGTCGTGGTACCATTTCTCAGGCACTATTAAAAAAA  
AACAGGCTGAGCAAGTGTCAAGGAGCAAGTCAGTGAGCAGCAGCCCTAATGATCTC  
TGCATCAGCTCCTGCCCTCAGGTTCCACCTATTGAGTTCTGTCCTAGCTCCCTA  
CACTGATGAACAATGATGTGGAAGTATAAGCCAATAATCCTTCTCCCCAACTT  
GCTGTTGGTCATGATGTTCATCACAGTGATAATTAGTCCTCATGAAGATGCTGGTGT  
TTATAACACCTTGGACTAAATTCTGTTATCTATAGCTGAGGAAAATGGAGCATAGA  
AACTCCAGACTACACCAGAGTGAACTCTGGGCTGAGCTAGAATCACACCCAC  
GTGCACTCCACTGCCGGGCTTCTAACCGGAACACAGTTGTAAGGAAATT  
GTTTGTGTTCCATTGACATGTGGACTTAATTGACGATTGTCAGTGAAAGCTGAAAATG  
ATTTTTTCCAGGTATAACAGCCTCACTAGATTGACAGAAAATGACTTTCTGGCCT  
GAGCAGACTGGAGTTACTCATGCTGCACAGCAATGGCATTGACAGAGTCAGTGACA  
AGACCTTCTCGGGCTGCACTGCTGCAGGTGAGATAGGTAGAGGGTGTGGAG  
TGAGAAGAGAGGGTCAACTGTGGGTATACCCAAAAGCTGCTGATTCCGTGGAG  
ACATTCTATAAGCATTCTATAAAACTAGAGGCAGATATCAAGGAAGGATTCAATTG  
AATGCAATTGAGAAAATTGAAATTAGAAAATGCTGGGGAAAATGCTTAC

ACAATTGCGAGGACCTAATTAGGATCTCCAATAGCCACATAAAAAGCACAGCATG  
GCGGCAGACACCTGCAATTCCCTGCCCTGGAAGCACCCTGTCAGAACATCCCAGAGACT  
CATTGGCAAACACTCTATTCAATCAATGAAGTCCATATTCACTGACAAAACITGAC  
TCAGAAACTAATGTGAAAGCATCAGGAAGACAGCCAACATCTGGTCTCTACTCAT  
GCATGAATAAGGGATCCCAGAGAGAAGGGAAAGAAAAAGGAAGGAAGGAAGGAAG  
GAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAGAGAGGGAGGGAGGAAGGAGGG  
AGGGAAAGGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG  
GAAAGGGGGAGAAAGAAGAGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG  
ACACCTTAAATTTATCCATAAAAGGTCAATTCCACCTGTTGTCTGGAAGTAGAGT  
GGGATCCCTATATAAGGGCAGTCCTAACATAGTAGCATTTATAAACCAATTACAA  
ATTTGAGTTTCTCTACTTTATCCTCTACCATCTCAAACACTGAAACTACAATTATT  
CCCACAAATGAAGAAAATGCTGTAAGAGTTTCACACACCGAAGTGGGAAACTTAA  
GGATTAGACAAGCTAACATGAGAATGGGAGAACAAAAAGAGACTGCACAGGG  
AGCCCTTCTGTTATAATCTTGACACTTGAGAAGCTAATTGACGCTGCATGACTA  
CTCAACTCTTAAGCAAACAATGCTGTTCATGAAAAGCACAATAAAGTACATAT  
GTCCCATAATATTCAAAATTGCACTGCAGCACATAATAGCAATCAAAGCAATAA  
CACCCACTGTCACAGAGACTTAAACATGAAACTGGAACTATGCTAGTGTGTTGA  
CTTAGGGTACATAGTATGCTGTCATGTTACCAATGTTGATTAGGTCACTCAGA  
CAGCATTGGAACATGTATCTCAGGAGGAATCATTGATGCTATCCTGCATGAAATT  
TCCACCTATGTTATTCTCTAGCCAGGTTCTGATGGAGAACATTGGGTTG  
AGGTTTACTCCCAGGTAAACATTAGGGAAAAGCTGTCTATGTTCTCAGTTGGCTT  
TATTATGAGGGATGTTGATTCCAGAAAATTCTCTTTGAAGAGATTACAATT  
GGTCAAACAGAAAATATGAAAAAGTTATTGTTTATTAGTATTGATGTTCTT  
TCTTTTAAATGGTATGCTTAGAACTAATTAAAGATTAGATTAGATTAGA  
AAATAATCAGAGAGGGATTGATGAATGCTAACAGCATGAAAAATTCAAATT  
TTGCTCTAATTCAATTGAGAACATTAAATTCTATTACTATAAAAGACAGCACGCCAG  
ATGTGTGCCAGCTGAGGAGTGGATAAACTGTGTAACGTGAGTGCTATGAGAAC  
GAAAGGAGTGAAGGGTTGATGTGCGCTGCAACATCTGAAAACATTGGCTACATG  
ATGGAAGCCAGGCACAAAAAGCCACATATTGATGGTTATGTTATATGAAATGTT  
AAAATACATGGATTCTAGCAAACAGAGTAAGATGTTACTTAGGGCAGGAGGAAG  
TTAAAAAAAAAAACTATTGATGTGGAATGATCTTAATTGGGAAAAGACAATT  
TCCTAAGACGAAATAGTGAGGTAGATATAGTTATATCCCTGTTGATATTGAA  
ACCAGCATGCTGCTGAGAAGGGCTAATGAAGGGCAGGAGGAAGTGAATG  
AGATGGTAGAAAGGAAAGTCATATACCATGGCTCTCGTGGGTGGAATCTAGAT  
ATGTTAATATATTGACATAAAGGAAGGAATTGTTAGGGAGGATCAAAACCAACA  
GGAGTGAGGGAGACAATAGGAACCAATGAGAGGCAAAGTCTGCAATGTGTT  
GGAGACACCATAATAAAACTCCTTTGTTGCTAACTAAAACCACTAAATCTAA  
AAACAAAACATTTCGACAAGAATTATTATTCAATAAAGATGTTAAATGGG  
GGAAGTTGAAGTCATTGATAGTCTCATAAACTTAAATGTATTAAACTGCTTTA  
CGTTTTTATTATTAAATTACTCTTGCTGTCATTATTATCATCATCATTATCGTCATCAT

CATCACTAATGCTTTCACCACACAAATGTAGGCAGAAGAGTGTAACTCCACTTAG  
TGAGGCAATCTGGAGAGGGAAAGGAAGCGGATGCCGGGCAGAGGCACACAGGAG  
GACAGTGAGAGGGAAATGAACAAGAAAAATGTGGACACATGCACAAAAATTCCA  
TAGTCCACTACATTACTTGTATTCTAATATTAAGAAAATAATAAAACCCATTCTGTG  
CACTTATCACCCAGGCTAACAGTTATCTGGCCACAGATCCTGTCTCACTGCATCCT  
GTCCACCTGAGTCCACTTAGCGTCTGAATCCAATCCAGGGCATGATGCTTACTCCT  
ACACAGAACTAAAGATTAAAGAGAGTTAAAAGTAACCATGACATCTCTGTTCCT  
TTAGCGATAAGTCTTAATATTATGGCTGCTGTATGTTCTAATTCTCTAATATT  
GTCACATTAGTGGCAACTACTTGTGAATTGAGTGGAGTTAAGGTCCCAG  
GATTAATCTCAACATATTCTATATTATAAACTTTCTCTTGTGAAAGTTCCCTT  
GAGAAAACAAATATGCCATATCTTCTTACAGGTCTAAAAATGAGCTATAACAA  
AGTCCAAATAATTGAGAAGGATACTTGTATGGACTCAGGAGCTGACCCGGTGCA  
CCTGGATCACACAAACATTGAGTTATCAACCCCCAGGCCTTACGGACTCACCTT  
GCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACAT  
TTGTCTCTTGAGCTATCTCCAGATATTAAAACCTCCTCATTAAGNACCTGTACTT  
GTATGATAACTTCATTGACCTCCCTCCAAAAGAAATGGTCTCCTCTATGCCAAACC  
TAGAAAGCCTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTAAAGTGGT  
TGTCCGAGTGGATGCAGGGAAACCCAGGTAACTATCTTGTGTTGTTCTTTTT  
ATARKACGTATTTCTCAATTCTATTAGAATGATATCCAAAAGTCCCCCATAACC  
TCCCCCCACTCCCTACCTACCCATTCCATTTTGGCCCTGGCATTCCCTGTACT  
GGGCATATAAAGTTGCGTGTCCAATGGACCTCTTCCAGTGTGATGGCCAAGTAG  
GCCATTTGATACATATGCAGCTAGAGTCAGAGCTCTGGGTACTGGTTAGTTC  
ATAATGTTGTTGCACCTACAGGGTGAA (SEQ ID NO:20)

Figure 51

MPKRAHWGALSVVLILLWGHPRVALACPACYPSEVHCTFRSLASVPAGIARHVE  
 RINLGFSIQALSETSFAGLTKELEMMIHNEIPSIPDGALRDLSSLQVFKFSYNKLRVITG  
 QTLQGLSNLMRLHIDHNKIEFIHPQAFNGLTSRLLHLEGNLLHQLHPSTFSTFTFLDYFR  
 LSTIRHLYLAENMVRTLPASMLRNMPLENLYLQGNPWTCDCEMRWFLEWDAKSRGIL  
 KCKKDKAYPEGGQLCAMCSPKKLYKHEHKLKDMTCLKPSIESPLRQNRSRSIEEQEQ  
 EEDGGSQQLILEKFQLPQWSISLNMTDEHGNMVNLVCDIKKPMVDVYKJHLNQTDPPDIDIN  
 ATVALDFECPMTRENEYEKWLKIAYYSEPVKLHREMLSKDPRVSYQYRQDAEEL  
 YYTGVRQAQILAEPPEWVMQPSIDIQLNRRQSTAKKVLLSYYTQYSQTISTKDTRQARGRS  
 WVMIEPSGAVQRDQTVLEGGPCQLSCNVKASESPSIFWVLPDGSILKAPMDDPSKFSIL  
 SSGWLRIKSMEPSDSGLYQCIAQVRDEMCRMVYRVLVQSPSTQPAEKDTVTIGKNPGES  
 VTLPCNALAIAPEAHLSWILPNRRJINDLANTSHVYMLPNGTLSIPKVQVSDSGYYRCAV  
 NQQGADHFTVGITVTKGSGLPSKRGRPGAKALSRVREDIVEDEGGSGMGDEENTSR  
 RLLHPKDQEVLKTKDDAINGDKAKGRRKLKLWKHSEKEPETNAEGRRVFESRR  
 INMANKQINPERWADILAKVRGKNLPKGTEVPLIKTTSSPPSLSLEVTPPFPAVSPPSASP  
 VQTVTSAEESSADVPLLGEHHVLGTISSASMGLEHNHNGVILVEPEVTSTPLEEVVDDL  
 SEKTEEITSTEGDLKGTAAPTLISEPYEPSPTLHTLDTVYEKPTHEETATEGWSAADVGSS  
 PEPTSSEYEPLDAVSLAESEPMQYFDPDLETKSQPDDEDKMKEDTFAHTPTPTIWVNDS  
 STSQLFEDSTIGEPGVPGQSHLQGLTDNIHLVKSSLSTQDTLLIKGMKEMSQTQGGNM  
 LEGDPTHRSSESEGQESKSITLPDSTLGIMSSMSPVKKPAETTVGTLKDTTVTTTPR  
 QKVAPSSTMSTHSRRRNPKFRHRHKQTPTTFAPSETFSTQPTQAPDIKISS  
 QVESSLVPTAWVDNTVNTPKQLEMEKNAEPTSKGTPRRKHGKRPNKHYTPSTVSSRA  
 SGSKPSPSPENKHRNIVTPSSETILLPRTVSLKTEGPYDSLDMYTTRKIYSSYPKVQETLP  
 VTYKPTSDGKEIKDDVATNVDKHKSILVTGESITNAIPTSRSLVSTMGEFKEESSPVGF  
 GTPTWNPSRTAQPGRLQTDIPVTTSGENLTDPPPLLKELEDVDFTEFLSSLTVSTPFHQEE  
 AGSSTTLSSIKVEVASSQAETTLDQDHLETTVAILLSETRPQNHTPTAARMKEPASSPS  
 TILMSLGQTTITKPALPSPRISQASRDSKENVFLNYVGNPETEATPVNNEGTQHMSGPNE  
 LSTPSSDRDAFNLSKLELEKQVFGSRSLPRGPDSQRQDGRVHASHQLTRVPAKPLPTA  
 TVRLPEMSTQSASRYFVTSQSPRHWTKPEITTPSGALPENKQFTPRLSSTIPLPLHM  
 SKPSIPSFKTDRRTDQFNGYSKVFGNNSIPEARNPVGKPPSPRIPHYSNGRLPFTNKTLSF  
 PQLGVTRRPQIPTSPAPVMRERKVIPGSYNRIHSHSTFHLDGFPPAPPLLHTPQTTGSPSTN  
 LQNIPMVSSTQSSISFITSSVQSSGSFHQSSSKFFAGGPPASKFWSLGEKPQILTQSPQTVSV  
 TAETDTVFPCEATGKPKPFVTWTKVSTGALMTPNTRIQRFEVLKNGTLVIRKVQVQDRG  
 QYMCTASNLHGLDRMVVLLSFTVQQPQILASHYQDVTVYLGDTIAMECLAKGTPAPQI  
 SWIFPDRRVWQTVPESRITLHENRTLSIKEASFSDRGVYKCVASNAAGADSLAIRLHV  
 AALPPVIHQEKLENISLPPGLSIHIHCTAKAAPLPSVRWVLGDTQIRPSQFLHGNLFVFP  
 NGTLYIRNLAPKDSGRYECVAANLVGSARRTVQLNVQRAAANARITGTSPRRTDVRYG  
 GTLKLDCSASGDPWPRLWRLPSKRMIDALFSFDSRIKVFANGTLVVKSVTDK

80/90

DAGDYLCAVNKGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCVATGL  
PNPEISWLPDGSLVNSFMQSDDSGGRTKRYVVFNNGTLYFNEVMREEGDYTCFAEN  
QVGKDEMVRVKVVTAPATIRNKTYLAQVVPYGDVVTVACEAKGEPMKPWTWLSPN  
KVIPTSSEKYQIYQDGTLIQLKAQRSDSGNYTCLVRNSAGEDRKTWVHNVQPPKING  
NPNPITTREIAAGGSRKLIIDCKAEGIPTPRVLWAFPEGVVLPAFYGNRITVHGNGSLDI  
RSLRKSDSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGHTISLNC  
AAGTPTPSLVWVLPNGTDLQSGQQQLQRFYHKADGMLHISGLSSVDAGAYRCVARNA  
GHTERLVSLKVGLKPEANKQYHNLVSIINGETLKLPCTPPGAGQGRFSWTLNGMHLEG  
PQTLGRVSLLDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPRITSEPTPVI  
YTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAGVQARLYGNRFLHPQGSLTIQHAT  
QRDAGFYKCMAKNILGSDSKTTYIHVF (SEQ ID NO: 21)

Figure 52

ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT  
 TTGGGGCCAT CCGCGAGTGG CGCTGGCCTG CCCGCATCCT TGTGCCTGCT  
 ACGTCCCCAG CGAGGTCCAC TGCACGTTCC GATCCCTGGC TTCCGTGCC  
 GCTGGCATTG CTAGACACGT GGAAAGAAC AATTGGGGT TTAATAGCAT  
 ACAGGCCCTG TCAGAAACCT CATTGCAGG ACTGACCAAG TTGGAGCTAC  
 TTATGATTCA CGGCAATGAG ATCCAAGCA TCCCCGATGG AGCTITAAGA  
 GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT  
 GATCACAGGA CAGACCCTCC AGGGTCTCTC TAACTTAATG AGGCTGCACA  
 TTGACCACAA CAAGATCGAG TTTATCCACC CTCAAGCTT CAACGGCTTA  
 ACGTCTCTGA GGCTACTCCA TTTGGAAGGA AATCTCCTCC ACCAGCTGCA  
 CCCCAGCACC TTCTCCACGT TCACATTIT GGATTATTC AGACTCTCCA  
 CCATAAGGCA CCTCTACTTA GCAGAGAAC TGGTTAGAAC TCTTCCTGCC  
 AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTACT TGCAGGGAAA  
 TCCGTGGACC TCGGATTGTG AGATGAGATG GTTTTGGAA TGGGATGCAA  
 AATCCAGAGG AATTCTGAAG TGTAAAAAGG ACAAAAGCTTA TGAAGGCGGT  
 CAGTTGTGTG CAATGTGCTT CAGTCCAAAG AAGTTGTACA AACATGAGAT  
 ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCATAA GAGTCCCC  
 TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG  
 GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAAGTGC CCCAGTGGAG  
 CATCTCTTGT AATATGACCG ACGAGCACCG GAACATGGTG AACTGGTCT  
 GTGACATCAA GAAACCAATG GATGTGTACA AGATTCACTT GAACCAAACG  
 GATCCTCCAG ATATTGACAT AAATGCAACA GTGCCITGG ACTTTGAGTG  
 TCCAATGACC CGAGAAAAT ATGAAAAGCT ATGAAATTG ATAGCATACT  
 ACAGTGAAGT TCCCCTGAAG CTACACAGAG AGTCATGCT CAGCAAAGAC  
 CCCAGAGTCA GCTACCAGTA CAGGCAGGAT GCTGATGAGG AAGCTCTTA  
 CTACACAGGT GTGAGAGCCC AGATTCTGC AGAACCAAGAA TGGGTCTGC  
 AGCCATCCAT AGATATCCAG CTGAACCGAC GTCAGAGTAC GGCCAAGAAG  
 GTGCTACTTT CCTACTACAC CCAGTATTCT CAAACAATAT CCACCAAAGA  
 TACAAGGCAG GCTCGGGCA GAAGCTGGGT AATGATTGAG CCTAGTGGAG  
 CTGTGCAAAG AGATCAGACT GTCCTGGAAG GGGGTCCATG CCAGTTGAGC  
 TGCAACGTGA AAGCTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA  
 TGGCTCCATC CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA  
 TTCTCAGCAG TGGCTGGCTG AGGATCAAGT CCATGGAGCC ATCTGACTCA  
 GGCTTGTACC AGTGCATTGC TCAAGTGAGG GATGAAATGG ACCGCATGGT  
 ATATAAGGGTA CTTGTGCAGT CTCCCTCCAC TCAGGCCAGCC GAGAAAGACA  
 CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT  
 GCTTAGCAA TACCCGAAGC CCACCTTAGC TGGATTCTTC CAAACAGAAG  
 GATAATTAAT GATTGGCTA ACACATCACA TGTATACATG TTGCCAAATG  
 GAACTCTTC CATCCCAAAG GTCCAAGTCA GTGATAGTGG

TTACTACAGA TGTGTGGCTG TCAACCAGCA AGGGGCAGAC CATTTACGG  
TGGGAATCAC AGTGACCAAG AAAGGGCTG GCTGCCATC CAAAAGAGGC  
AGACGCCAG GTGCAAAGGC TCTITCCAGA GTCAGAGAAG ACATCGTGG  
GGATGAAGGG GGCTCGGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC  
TTCTGCATCC AAAGGACCAA GAGGTGITCC TCAAAACAAA GGATGATGCC  
ATCAATGGAG ACAAGAAAGC CAAGAAAGGG AGAAGAAAGC TGAAACTCTG  
GAAGCATTG GAAAAAGAAC CAGAGACCAA TGTGCAGAA GGTGCGAGAG  
TGTTGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAATCCG  
GAGCGCTGGG CTGATATTTC AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA  
GGGCACAGAA GTACCCCCGT TGATTAAAAC CACAAGTCCT CCATCCTTGA  
GCCTAGAAGT CACACCACCT TTTCCTGCTG TTTCTCCCCC CTCAGCATCT  
CCTGTGCAGA CAGTAACCAAG TGCTGAAGAA TCCTCAGCAG ATGTACCTCT  
ACTTGGTGAA GAAGAGCACG TTTGGGTAC CATTCCCTCA GCCAGCATGG  
GGCTAGAACAA CAACCACAAAT GGAGTTATTC TTGTTGAACC TGAAGTAACA  
AGCACACCTC TGAGGAAGT TGTTGATGAC CTTTCTGAGA AGACTGAGGA  
GATAACTTCC ACTGAAGGAG ACCTGAAGGG GACAGCAGCC CCTACACTTA  
TATCTGAGCC TTATGAACCA TCTCTACTC TGCACACATT AGACACAGTC  
TATGAAAAGC CCACCCATGA AGAGACGGCA ACAGAGGGTT GGTCTGCAGC  
AGATGTTGGA TCGTCACCAAG AGCCCACATC CAGTGAGTAT GAGCCTCCAT  
TGGATGCTGT CTCCCTGGCT GAGTCTGAGC CCATGCAATA CTTTGACCCA  
GATTGGAGA CTAAGTCACA ACCAGATGAG GATAAGATGA AAGAAGACAC  
CTTGCACAC CTTACTCCAA CCCCCACCAT CTGGGTTAAT GACTCCAGTA  
CATCACAGTT ATTGAGGAT TCTACTATAG GGGAACCAAGG TGTCCCAGGC  
CAATCACATC TACAAGGACT GACAGACAAC ATCCACCTG TGAAAAGTAG  
TCTAAGCACT CAAGACACCT TACTGATTAA AAAGGGTATG AAAGAGATGT  
CTCAGACACT ACAGGGAGGA AATATGCTAG AGGGAGACCC CACACACTCC  
AGAAGTTCTG AGAGTGAGGG CCAAGAGAGC AAATCCATCA CTTTGCTGA  
CTCCACACTG GGTATAATGA GCAGTATGTC TCCAGTTAAG AAGCCTGCAG  
AAACCCACAGT TGTACCCCTC CTAGACAAAG ACACCCACAAG AGTAACAACA  
ACACCAAGGC AAAAAGTTGC TCCGTACATCC ACCATGAGCA CTCACCCCTC  
TCGAAGGAGA CCCAACGGGA GAAGGAGATT ACGCCCCAAC AAATTCCGCC  
ACCGGCACAA GCAAACCCCA CCCACAACCTT TTGCCCCATC AGAGACTTTT  
TCTACTCAAC CAACTCAAGC ACCTGACATT AAGATTCAA GTCAAGTGG  
GAGTTCTCTG GTTCTACAG CTTGGGTGGA TAACACAGTT AATACCCCCA  
AACAGTTGGA AATGGAGAAG AATGCAGAAC CCACATCCAA GGGAACACCA  
CGGAGAAAAC ACGGGAAGAG GCAAACAAA CATCGATATA CCCCTCTAC  
AGTGAGCTCA AGAGCGTCCG GATCCAAGCC CAGCCCTTCT CCAGAAAATA  
AACATAGAAA CATTGTTACT CCCAGTTCAAG AACTATACT TTTGCCTAGA  
ACTGTTCTC TGAAAAGTGA GGGCCCTAT GATTCCCTAG ATTACATGAC  
AACCACCAAGA AAAATATATT CATCTTACCC TAAAGTCCAA GAGACACTTC  
CAGTCACATA

TAAACCCACA TCAGATGGAA AAGAAATTAA GGATGATGT GGCACAAATG  
 TTGACAAACA TAAAAGT GAC ATTTAGTCA CTGGTGAATC AATTACTAAT  
 GCCATACCAA CTTCTCGCTC CTTGGTCTCC ACTATGGGAG AATTAAAGGA  
 AGAACCTCT CCTGTAGGCT TTCCAGGAAC TCCAACCTGG AATCCCTCAA  
 GGACGGGCCA GCCTGGGAGG CTACAGACAG ACATACCTGT TACCACTTCT  
 GGGGAAAATC TTACAGACCC TCCCCTTCTT AAAGAGCTTG AGGATGTGGA  
 TTTCATTCC GAGTTTTGT CCTCTTGAC AGTCTCCACA CCATTTCACC  
 AGGAAGAACG TGTTCTTCC ACAACTCTCT CAAGCATAAA AGTGGAGGTG  
 GCTCAAGTC AGGCAGAAC CACCACCTT GATCAAGATC ATCTTGAAAC  
 CACTGTGGCT ATTCTCCTTT CTGAAACTAG ACCACAGAAT CACACCCCTA  
 CTGCTGCCG GATGAAGGAG CCAGCATCCT CGTCCCCATC CACAATTCTC  
 ATGTCTTGG GACAAACAC CACCACTAAG CCAGCACTTC CCAGTCCAAG  
 AATATCTCAA GCATCTAGAG ATTCCAAGGA AAATGTTTC TTGAATTATG  
 TGGGAATCC AGAAACAGAA GCAACCCAG TCAACAATGA AGGAACACAG  
 CATATGTCAG GCCAAATGA ATTATCAACA CCCTCTTCCG ACCGGGATGC  
 ATTAACTTG TCTACAAAGC TGGATTGGA AAAGCAAGTA TTTGGTAGTA  
 GGAGTCTACC ACGTGGCCA GATAGCCAAC GCCAGGATGG AAGAGTTCAT  
 GCTCTCATC AACTAACCAAG AGTCCCTGCC AAACCCATCC TACCAACAGC  
 AACAGTGAGG CTACCTGAAA TGTCACACAA AAGCGCTTCC AGATACTTIG  
 TAACCTCCA GTCACCTCGT CACTGGACCA ACAAACCGGA AATAACTACA  
 TATCCTCTG GGGCTTGCAG AGAGAACAAA CAGTTACAA CTCCAAGATT  
 ATCAAGTACA ACAATTCCCTC TCCCATTGCA CATGTCCAAA CCCAGCATT  
 CTAGTAAGTT TACTGACCGA AGAACTGACC AATTCAATGG TTACTCCAAA  
 GTGTTGGAA ATAACAACAT CCCTGAGGCA AGAAACCCAG TTGGAAAGCC  
 TCCCAGTCCA AGAATTCCCTC ATTATTCCAA TGGAAGACTC CCTTCTTIA  
 CCAACAAAGAC TCTTCTTCC CACAGTTGG GAGTCACCCG GAGACCCAG  
 ATACCCACTT CTCCTGCCAG AGTAATGAGA GAGAGAAAAG TTATTCCAGG  
 TTCCTACAAC AGGATACATT CCCATAGCAC CTTCCATCTG GACTTTGGCC  
 CTCCGGCACC TCCGTTGTG CACACTCCGC AGACCACGGG ATCACCCCTA  
 ACTAACTTAC AGAATATCCC TATGGTCTCT TCCACCCAGA GTTCTATCTC  
 CTTTATAACA TCTTCTGTCC AGTCTCAGG AAGCTTCCAC CAGAGCAGCT  
 CAAAGTTCTT TGCAGGAGGA CCTCCTGCAT CCAAATTCTG GTCTTTGGG  
 GAAAAGCCCC AAATCCTCAC CAAGTCCCCA CAGACTGTGT CCGTCACCGC  
 TGAGACAGAC ACTGTGTTCC CCTGTGAGGC AACAGGAAAA CCAAAGCCTT  
 TCGITACTTG GACAAAGGTT TCCACAGGAG CTCTTATGAC TCCGAATACC  
 AGGATACAAC GGTGAGGT TCTCAAGAAC GGTACCTTAG TGATACGGAA  
 GGTCAAGTA CAAGATCGAG GCCAGTATAT GTGCACCGCC AGCAACCTGC  
 ACGGCCTGGA CAGGATGGTG GTCTTGCTT CGGTACCGGT GCAGCAACCT  
 CAAATCCTAG CCTCCCACTA CCAGGACGTC ACTGTCTACC TGGGAGACAC  
 CATTGCAATG GAGTGTCTGG CCAAAGGGAC CCCAGCCCC CAAATTCCCT  
 GGATCTTCCC TGACAGGAGG GTGTGGAAA CTGTGTCCCC

CGTGGAGAGC CGCATCACCC TGCACGAAAA CCGGACCCTT TCCATCAAGG  
AGGCGTCCTT CTCAGACAGA GGCCTCTATA AGTGCCTGGC CAGCAATGCA  
GCCGGGGCGG ACAGCCTGGC CATCCGCCTG CACGTGGCGG CACTGCC  
CGTTATCAC CAGGAGAAC TGAGAACAT CTCGCTGCC CCGGGGCTCA  
GCATTACAT TCACTGCCTG GCCAAGGCTG CGCCCTGCC CAGCGTGC  
TGGGTGCTCG GGGACGGTAC CCAGATCCGC CCCTCGCAGT TCCTCCACGG  
GAACTTGTTT GTTTCCCCA ACGGGACGCT CTACATCCGC AACCTCGCG  
CCAAGGACAG CGGGCGCTAT GAGTGCCTGG CCGCCAACCT GGTAGGCTCC  
GCGCGCAGGA CGGTGCAGCT GAACGTGCAG CGTGCAGCAG CCAACGCG  
CATCACGGC ACCTCCCCGC GGAGGACGGA CGTCAGGTAC GGAGGAACCC  
TCAAGCTGGA CTGCAGCGCC TCGGGGGACC CCTGGCCCG CATCCTCTGG  
AGGCTGCCGT CCAAGAGGAT GATCGACCGC CTCTCAGTT TTGATAGCAG  
AATCAAGGTG TTTGCCAATG GGACCCTGGT GGTGAAATCA GTGACGGACA  
AAGATGCCGG AGATTACCTG TCGTAGCTC GAAATAAGGT TGGTGATGAC  
TACGTGGTGC TCAAAGTGGA TGTGGTGATG AAACCGGCCA AGATTGAACA  
CAAGGAGGAG AACGACCACA AAGTCTCTA CGGGGGTGAC CTGAAAGTGG  
ACTGTGTGGC CACCGGGCTT CCCAATCCCG AGATCTCCTG GAGCCTCCCA  
GACGGGAGTC TGGTGAACCTC CTTCATGCAG TCGGATGACA GCGGTGGACG  
CACCAAGCGC TATGTCGTCT TCAACAATGG GACACTCTAC TTTAACGAAG  
TGGGGATGAG GGAGGAAGGA GACTACACCT GCTTGCTGA AAATCAGGTC  
GGGAAGGACG AGATGAGAGT CAGAGTCAAG GTGGTGACAG CGCCGCCAC  
CATCCGGAAC AAGACTTACT TGGCGGTTCA GGTGCCCTAT GGAGACGTGG  
TCACTGTAGC CTGTGAGGCC AAAGGAGAAC CCATGCCAA GGTGACTTGG  
TTGTCCCCAA CCAACAAGGT GATCCCCACC TCCTCTGAGA AGTATCAGAT  
ATACCAAGAT GGCACCTCTCC TTATTCAAGAA AGCCCAGCGT TCTGACAGCG  
GCAACTACAC CTGCCTGGTC AGGAACAGCG CGGGAGAGGA TAGGAAGACG  
GTGTGGATTC ACGTCAACGT CCAGCCACCC AAGATCAACG GTAACCCCAA  
CCCCATCACC ACCGTGCGGG AGATAGCAGC CGGGGGCAGT CGGAAACTGA  
TTGACTGCAA AGCTGAAGGC ATCCCCACCC CGAGGGTGT ATGGGCTTTT  
CCCGAGGGTG TGGTCTGCC AGCTCCATAC TATGGAAACC GGATCACTGT  
CCATGGCAAC GGTTCCCTGG ACATCAGGAG TTTGAGGAAG AGCGACTCCG  
TCCAGCTGGT ATGCATGGCA CGAACGAGG GAGGGGAGGC GAGGTTGATC  
GTGCAGCTCA CTGTCCTGGA GCCCATGGAG AAACCCATCT TCCACGACCC  
GATCAGCGAG AAGATCACGG CCATGGCGGG CCACACCATC AGCCTCAACT  
GCTCTGCCGC GGGGACCCCG ACACCCAGCC TGGTGTGGGT CCTTCCCAAT  
GGCACCGATC TGCAGAGTGG ACAGCAGCTG CAGCGCTCT ACCACAAGGC  
TGACGGCATG CTACACATTA GCGGTCTCTC CTCGGTGGAC GCTGGGCCT  
ACCGCTGCGT GGGCCGCAAT GCCGCTGGCC ACACGGAGAG GCTGGTCTCC  
CTGAAGGTGG GACTGAAGCC AGAAGCAAAC AAGCAGTATC ATAACCTGGT  
CAGCATCATC AATGGTGAGA CCCTGAAGCT CCCCTGCACC CCTCCCCGGG  
CTGGGCAGGG ACGTTCTCC TGGACGCTCC CCAATGGCAT GCATCTGGAG

GGCCCCCAAA CCCTGGGACG CGTTTCTCTT CTGGACAATG GCACCCTCAC  
GGTCGTGAG GCCTCGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG  
AGACGGAGTA CGGCCCTCG GTCACCAGCA TCCCCGTGAT TGTGATGCC  
TATCCTCCCC GGATCACCAAG CGAGCCCACC CCGGTACACT ACACCCGGCC  
CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT CCCAAAGCTG  
ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTCA  
GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCCAGGGAT CACTGACCAT  
CCAGCATGCC ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGAAAAAA  
ACATTCTCGG CAGTGACTCC AAAACAACCT ACATCCACGT CTTCTGAAAT  
GTGGATTCCA GAATGATTGC TTAGGAACTG ACAACAAAGC GGGGTTGTA  
AGGGAAAGCCA GTTGGGGAA TAGGAGCTCT TAAATAATGT GTCACAGTGC  
ATGGTGGCCT CTGGTGGGT TCAAGTTGAG GTTGATCTT ATCTACAATT  
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT  
GAGACACTT CTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAAGGGTG  
TCTGTGCTCT GACTGCAATT TTTCTTCTT TGCAAATGCC ACTCGACTGC  
CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCACTCA AAAATAAGCC  
ATAGACATGA ACAACACCTC ACTACCCAT TGAAAGACGCA TCACCTAGTT  
AACCTGCTGC AGTTTITACA TGATAGACTT TGTTCCAGAT TGACAAGTCA  
TCITTCAGTT ATTCCTCTG TCACCTCAAA ACTCCAGCTT GCCCAATAAG  
GATTAGAAC CAGAGTGA CAGATATATA TATATATTAA ATTCAAGAGT  
TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTCTTCC  
TGGAACTCAC TTTTATATA ATGTTTATA TATATATTAA TTCCTTCAA  
ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT ATAAAATTA  
ATAAATTATT GGTCTTACA AGACTTGGAT ACATTACAGC AGACATGGAA  
ATATAATTAA AAAAATTTC TCTCCAACCT CCTCAAATT CAGTCACCAC  
TGTTATATTA CCTTCTCCAG GAACCCCTCCA GTGGGGAAAGG CTGCGATATT  
AGATTCCTT GTATGCAAAG TTTTGTGA AAGCTGTGCT CAGAGGAGGT  
GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACCTTACAG AATTGAATCT  
AGAGTCTTCC CCGAAAAGCC CAGAAACTTC TCTGCAGTAT CTGGCTTGTG  
CATCTGGTCT AAGGTGGCTG CTTCTCCCC AGCCATGAGT CAGTTGTGC  
CCATGAATAA TACACGACCT GTTATTCCA TGACTGCTT ACTGTATTAA  
TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCAAAAAA AAAAAA

Figure 53

Human OCP: nucleotide sequence of ORF

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTGGTCTCCTTGCTGTGATCTGC  
 CTGGTCGCCACCCCTGGGGCAAGGCCTGCTCGCCGCTGCTGTTATATGCCT  
 ACGGAGGTACACTGCACATTCCGGTACCTGACTTCCATCCAGACAGCATCCGCC  
 AATGTGGAACGCATCAATTAGGATAAACAGCTGGTAGATTGATGGAAACAGAT  
 TTTTCTGGCCTGACCAAACGGAGTTACTCATGCTCACAGCAATGGCATTACACA  
 ATCCCTGACAAGACCTCTCAGATTGCAGGCCTGCAGGTCTTAAAAATGAGCTAT  
 AATAAAGTCCGAAAACCTCAGAAAGATACTTTATGGCCTCAGGAGCTGACACGA  
 TTGCACATGGACCACAACAATTGAGTTATAAACCCAGAGGTTTTATGGGCTC  
 AACATTCTCCGCCTGGTGCACTTGGAAAGGAAATCAGCTCACTAAGCTCCACCCAGAT  
 ACATTGTCTCTTGAGCTACCTCCAGATATTAAAATCTCTTCAAGTTCCTA  
 TACTGTCTGATAACTCCTGACCTCCCTCCCTCAAGAGATGGTCTCCTATATGCCT  
 GACCTAGACAGCCTTACCTGCATGGAAACCCATGGACCTGTGATTGCCATTAAAG  
 TGGTTGTCTGACTGGATACAGGAGAACAGCAGATGTAATAAAATGCAAAAAGATAGA  
 AGTCCCTCTAGTGCTCAGCAGTGTCCACTTGCATGAAACCTAGGACTTCTAAAGGC  
 AAGCCGTTAGCTATGGTCTCAGCTGCAGCTTCCAGTGTGCCAAGCCAACCATTGAC  
 TCATCCCTGAAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTCATC  
 TCTCCCCAAGGTTCATGGCACCCCTTGGCTCCCTCACTTGAATATGACAGATCAG  
 TCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAGCCCTCAAGGACATCACCC  
 ATTGCATTCACTGAAGAAAATGACTACATCGTGCTAAATACTCATTCAACATT  
 TTGGTGTGCAACATAGATTACGGTCACATTCAAGCCAGTGTGGCAAATTGGCTTG  
 TACAGTGATTCTCCTCTGATAACTAGAAAGGAGCCACTTGCTTAGTGAACACCCGCAG  
 CTCTATTACAAATATAAACAGGTGGCTCTAACGCTGAAGACATTAAACATA  
 GAGGCAGATCTCAGAGCAGATCCCTCTGGTTAATGCAAGACCAAATTCCCTGCAG  
 CTGAACAGAACTGCCACCACATTCACTGACATTACAGATCCAGTACTCCAGTGTGCT  
 CAAATCACTTACCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGACTATGATT  
 TCAAGGGATAACAATACTAAGCTGGAACATACTGTCTGGTAGGTGGAACCGTTGGC  
 CTGAACTGCCAGGCCAAGGAGACCCCACCCACACGTGGATTGGCTTAGCTGAT  
 GGAAGTAAAGTGAGAGGCCCTATGTCAGTGAGGATGGACGGATCTAACAGACAAA  
 AGTGGAAAATTGGAACTCCAGATGGCTGATAGTTGACACAGCGTATATCACTGT  
 ATAAGCAGCAATTATGATGATGCAGATATTCTCACCTATAGGATAACTGTGGTAGAA  
 CCTTGGTCGAAGCCTATCAGGAAATGGGATTCATCACACAGTTTCATTGGTGA  
 ACACTTGATCTCCATGCCATTCTACTGGTATCCCAGATGCCCTATTAGCTGGTT  
 ATTCCAGGAAACAATGTGCTCTACAGTCACCCGAAAGACCAAGGTTATTACGCTGTG  
 GGCACATTAAGAATATTACAGGTACCCGAAAGACCAAGGTTATTACGCTGTG  
 GCAGCCAACCCATCAGGGTTGATTTTGATTTCCAAGTTCACTGCAAGATGAAA  
 GGACAAAGGCCCTGGAGCATGGAGAAACAGAGGGATCTGGACTTGATGAGTCC  
 AATCCTATTGCTCATCTAACGGAGCCACCAGGTGCACAACCTCCGTACATCTGCTCTG  
 ATGGAGGCTGAGGTTGAAAACACACCTCAAGCACAAGTAAGAGGCACAACATACGG  
 GAATTAACACTCCAGCGACGTGGAGATTCAACACATCGACGTTTAGGGAGAATAGG  
 AGGCATTCCCTCCCTGCTAGGAGAATTGACCCACAACATTGGGCGGGACTGTTG  
 GAGAAAGCTAAAAGAATGCTATGCCAGACAAGCGAGAAAATACCACAGTGAGGCCA  
 CCCCCAGTGGTCACCCAACTCCAAACATACCTGGTGAAGAAGACGATTCCCTCAGGC  
 ATGCTCGCTCATGAGGAATTATGGTCCGGCACTAAAGCTTGAACCTCCA  
 GCAAGGACAGTGACTGCTGACTCCAGAACAAATCTGATAGTCCTATGACAAACATA  
 AATTATGGCACAGAATTCTCTCTGTTGTAATTCAAATACTACCACCTGAAGAA  
 CCCACAGATTCAAACGTCTACTGCTATTAAACTACAGCCATGTCAAAGAATATA

AACCCAACCATGTCAAGCCAAATAACAAGGCACAACCAATCAACATTCACTCCACTGTC  
 TTTCCACTGCTACTTGGAGCAACTGAATTTCAGGACTCTGACCAGATGGGAAGAGGA  
 AGAGAGCATTCAAAGTAGACCCCCAATAACAGTAAGGACTATGATCAAAGATGTC  
 AATGTCAAAATGCTTAGTAGCACCAACAAACTATTATTAGAGTCAGTAATACC  
 ACAAAATAGTCATCAGACATCTGTAAGAGAAGTGAGTGAAACCAGGCACAATCACTTC  
 TATTCTCACACTACTCAAATACTTAGCACCTCCACGTTCCCTCAGATCCACACACA  
 GCTGCTCATTCTCAGTTCCGATCCCTAGAAAATAGTACAGTTAACATCCCCTGTT  
 AGACGCTTGGGAGGGAGAGGAAAATTGGCGGAAGGGGGGGATTATCAGCCCATAT  
 AGAACTCCAGTTCTGCGACGGCATAGATAACAGCATTTCAGGTCAACAACCAGAGGT  
 TCTTCTGAAAAAAGCACTACTGCATTCTCAGCCACAGTGCTCAATGTGACATGTCTG  
 TCCTGTCTCCAGGGAGAGGCTCACCACTGCCACAGCAGCATTGTCATTCCAAAGT  
 GCTGCTCCCATCACCTCCCCAAAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCT  
 ACAACTCTAGTCCAGAATCCACTATTACTACTTGAGAACAAACCCAGTGTAGAGAAA  
 ACAACACCCACAATAAAATATTCAAGGACTGAAATTCCAAGTGACTIONCCAACGGT  
 GCAGTCATGACATATGCTCAAACATCCATACCCATGAAAAAAACTCACAAAGTAAAC  
 GCCAGTTACCCACGTGTCTAGCACCAATGAAGCTAAAGAGATTCACTGATTACA  
 TCGTCACTTCAGGTGCTATCACCAGCCACCAATGACTATTATAGCCATTACAAGG  
 TTTCAAGAAGGAAAATTCCCTGGCAACAGAACCTTGTAAATAACCATAACCCAAA  
 GGCAGATTAAGGAATCAACATAAGTTAGTTACAAAAAAGCACAGCTGTGATGCTT  
 CCTAAAACATCTCCTGCTTACACAGAGACAAAGTCCCTTCCATTCAACCA  
 CTTCAACAAAGTGTGATGCAAATTCCATCTAACCTTGACTACCGCTCACCAACT  
 ACGACCAAAACACACAATCCTGGAAGTCTCCAACAAAGAAGGAGCTCCCTCCA  
 CCCCTTAACCCATGCTCTAGTATTATAAGCAAAGACTCAAGTACAAAAGCATC  
 ATATCAACGCAAACAGCAATACCAGCAACAACCTCTACCTCCCTGCATCTGTCATC  
 ACTTATGAAACCAAACAGAGAGATCTAGAGCACAAACAATACAAAGAGAACAGGAG  
 CCTCAAAAGAAGAACAGGACTGACCCAAACATCTCCAGACCAGAGTTCTGGCTTC  
 ACTACACCCACTGCTATGACACCTCTGCTCTGGCATTCACTCATTCCCCACCAGAA  
 AACACAACCTGGATTCAAGCACAATCAGTTTCAAGAACCTTAATCTGACA  
 GATGTGATTGAAGAACTAGCCCAAGCAAGTACTCAGACTTTGAAGAGCACAAATTGCT  
 TCTGAAACAACTTGTCCAGCAATCACACCAGACTACACAACTAGGAAAGCATCA  
 TTAGACACTCCCATAACCACCATCTTGAGCAGCAGTGCTACTCTAACATGCCAGTCCC  
 ATCTCCCTCCCTTACTCAGAGAGCAGTTACTGACACACGTGGCAGTCCATTTC  
 CGGCTTATGACAAATACAGTGGCAAGCTGCACGAATCCTCAAGGCACAATCTCAA  
 ATGCCAAGTTCACAAITGGAACCACTCACTCATCTACCTCTAACATGTTACATTCT  
 ACTCCCATGCCAGCACTAACACAGTTAAATCACAGAACCTCAAATTCACTCCATCT  
 CCCTGGGAGAACATACCAATTGGCACAAACCAACTCAGACATTGCTGAAAAGGC  
 AAAAGCCAGAAGTAAGCATGTTGGCTACTACAGGCCGTGCGAGGCCACCACTCTT  
 GTTTCAGATTGGGATGGACAGAACACAAAGAACAGAGTGACTTTGATAAGAAACCA  
 GTTCAAGAAGCAACAACTTCCAAACTCCTCCCTTGACTCTTGCTAGGTATATA  
 TTTGAAAAGCCAGGATAGTTGGAGGAAAGCTGCAAGTTTACTATTCCAGCTAAC  
 TCAGATGCCATTCTCCCTGTGAAGCTGTTGGAAATCCCTGCCACCAATTCTATTGG  
 ACCAGAGTTCAAGGACTTGATTATCTAGAGGAAACCAAGAACAGCAGGGTCCAGGTT  
 CTCCCAATGGTACCCGTCCATCCAGAGGGTGGAAATTCAAGGACCGCGGACAGTAC  
 TTGTGTTCCGCATCCAATCTGTTGGCACAGACCACCTCATGTCACCTTGTCTGTG  
 GTTTCCTATCCTCCAGGATCCTGGAGAGACGTACCAAAGAGATCACAGTCTATTCC  
 GGAAGCACTGTGGAACTGAAGTGCAGAGCAGAACAGGTAGGCCAAGCCCTACAGTTAC  
 TGGATTCTGCAAACAAACAGTTGTCTCAGAACATCCCAGGGAAAGTAGGCAGGCT  
 GTGGTGACGGTTGACGGAACATTGGCTCCACAACTCTAGTATTATGACCGTGGC  
 TTTTACAAATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCACTGCTGGTTAAAATA  
 CAAGTCATTGCAGCACCACTGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGC  
 ACTTGGGTGAAAGTTAAAACCTGCCCTGACTGCAAAAGGAACCTCCAGCCAGC

GTTTACTGGGTCTCTGATGGCACTGAAGTGAAACCATTACAGTTACCAATTCC  
 AAGTTGTTCTTATTTCAAATGGGACTTGTATATAAGAAACCTAGCCTTCAGAC  
 AGGGGCACTTATGAATGCATTGCTACCAGTCCACTGGTCGGAGCGAAGAGTAGTA  
 ATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGATAGAACGTCATCCCAGAAA  
 AGGACTGAAGTGAATTGGGGACAAATTACTACTGAACTGCTCAGCCACTGGGGAG  
 CCCAAACCCCAAATAATGTGGAGGTACCATCCAAGGCTGTGGCGACCAGTGGAGC  
 TGGATCCACGTCTACCTAATGGATCCCTGTTATTGGATCAGTAACAGAAAAAGAC  
 AGTGGTGTCTACTTGTGTGGCAAGAAACAAATGGGGATGATCTGATACTGATG  
 CATGTTAGCCTAAGACTGAAACCTGCCAAATTGACCACAAGCAGTATTTAGAAAG  
 CAAGTGCTCCATGGGAAAGATTCCAAGTAGATTGCAAAGCTCCGGCTCCCCAGTG  
 CCAGAGATATCTGGAGTTGCCTGATGGAACCATGATCAACAATGCAATGCAAGCC  
 GATGACAGTGGCCACAGGACTAGGAGATACCCCTTCAACAATGGAACCTTATAC  
 TTCAACAAAGTTGGGGTAGCGGAGGAAGGAGATTATACTGCTATGCCAGAACACC  
 CTAGGGAAAGATGAAATGAAGGTCCACTTAACAGTTATAACAGCTGCTCCCCGGATA  
 AGGCAGAGTAACAAAACCAACAAGAGAATCAAAGCTGGAGACACAGCTGTCCTGAC  
 TGTGAGGTCACTGGGGATCCAAACCAAAATATTTGGTTGCTGCCCTCCAATGAC  
 ATGATTTCCCTCCATTGATAGGTACACATTCTGATGCCAATGGGTCTTGACCATC  
 AACAAAGTGAAACTGCTCGATTCTGGAGAGTACGTATGTTAGGCCGAAATCCAGT  
 GGGGATGACACCAAAATGTACAAACTGGATGTGGTCTCTAAACCTCCATTAATCAAT  
 GGTCTGTATACAAACAGAACTGTTATTAAAGCCACAGCTGTGAGACATTCAAAAAAA  
 CACTTTGACTGCAGAGCTGAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCA  
 GACAATATTTCTCACAGCCCCATACTATGGAAGCAGAACATCACAGTCCATAAAAAT  
 GGAACCTGGAAATTAGGAATGTGAGGCTTCAGATTAGCCGACTTTATCTGTGTG  
 GCCCGAAATGAAGGTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAAATG  
 CTGAGAAGACCGACATTAGAAATCCATTAAATGAAAAAAATAGTTGCCAGCTGGGAA  
 AAGTCCACAGCATTGAATTGCTCTGTTGATGGTAACCACCCACCTGAAATAATCTGG  
 ATTTACCAAATGGCACACGATTTCCAATGGACCACAAAGTTATCAGTATCTGATA  
 GCAAGCAATGGTTCTTTATCATTCTAAAACAACTCGGGAGGATGCAGGAAAATAT  
 CGCTGTGCAGCTAGGAATAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATT  
 GCCCAGAAGCCAGTTATTCTACCTATGCACCAGGGACAGTAAAGGCATCAGTGGAA  
 GAATCTCTATCACTGCATTGTGTCTGATGGAATCCCTAACGGCAAATATCAAATGG  
 ACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAAATGGGAAATACATATTG  
 CATGACAATGGCACCTAGTCATTAAGAAGCAACAGCTTATGACAGAGGAAACTAT  
 ATCTGTAAGGCTAAAATAGTGTGGTCATACACTGATTACTGTTCCAGTAATGATT  
 GTAGCCTACCCCTCCCCGAATTACAAATCGTCCACCCAGGAGTATTGTCACCAGGACA  
 GGGGCAGCCTTCAGCTCCACTGTGTGGCTTGGAGTTCCAGGCCAGAAATCACA  
 TGGGAGATGCCTGACCAACTCCCTCTCAACGGCAAGTAAAGAGAGGACACATGGAA  
 AGTGAGCAGCTTCACTTACAAGGTACCCCTAGTCATTAGAACATCCCCAAACCTCCGAT  
 TCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGTATTATGCAGCAACG  
 TATATTCAAGTAATCTGA

Figure 54 Human OCP: predicted amino acid sequence

MVKGRGIRTC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS  
 IPDSIPPNE RINLGYNSLV RLMETDFSL TKLELLMLHS NGIHTIPDKT  
 FSDLQALQL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY  
 GLNFLRLVHL EGNQLTKLHP DTFVSLSYLQ IFKISFIKFL YLSDNFLTSL  
 PQEMVSYMPD LDSLYLHGNP WTCDCHLKWL SDWIQEKPDV IKCKKDRSPS  
 SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS  
 SAFISPQGFM APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND  
 YIVLNNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL  
 YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI  
 QYSSDAQITL PRAEMRPVKH KWTMISRDNN TKLEHTVLVG GTVGLNCPGQ  
 GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH  
 CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI  
 PDASISWVIP GNNVLYQSSR DKVVLNNGL RILQVTPKDQ GYYRCVAANP  
 SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT  
 SALMEAEVGK HTSSTSKRHN YRELTQLRRG DSTHRRFREN RRHFPPSARR  
 IDPQHWAALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML  
 ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYGT EFSPVVNSQI  
 LPPEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA  
 TEFQDSDQMG RGREHFQSRP PITVRTMIKD VNVKMLSSTT NKLLLESVNT  
 TNSHQTSVRE VSEPRHNHY SHTTQILSTS TFPSDPHTAA HSQFPIPRNS  
 TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRYSIFR STTRGSSEKS  
 TTAFSATVNL VTCLSCLPRE RLTTATAALS FPSAAPITFP KADIARVPSE  
 ESTTLVQNPL LLLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTSI  
 PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR  
 RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF  
 HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMLPS  
 IIISKDSSTKS IIISTQTAIPA TTPTFPASVI TYETQTERSR AQTIQREQEP  
 QKKNRTDPNI SPDQSSGF TTPTAMTPPALA FTHSPPENTT GISSTISFHS  
 RTLNLTDVIE ELAQASTQTL KSTIASSETT SSKSHQSTTT RKASLDTPIP  
 PFLSSSATLM PVPISPPFQ RAVTDTRGDS HFRLMTNTVV KLHESSRHNL  
 QMPSSQLEPL TSSTSNNLHS TPMALTTVK SQNSKLTPSP WAEYQFWHKP  
 YSDIAEKGKK PEVSMMLATTG LSEATTLVSD WDGGQKNTKKS DFDKKPVQEA  
 TTSKLLPFDS LSRYIFEKPR IVGGKAASF IPANSDAFLP CEAVGNPLPT  
 IHWTRVSGLD LSRGNQNSRV QVLPNGTLSI QRVEIQDRGQ YLCASASNLF  
 TDHLHVTLSV VSYPPIRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI  
 LANQTVVSES SQGSRQAVVT VDGTLVLHNL SIYDRGFYKC VASNPQGQDS  
 LLVKIQVIAA PPVILEQRRQ VIVGTVGESL KLPCTAKGTP QPSVYWVLSD  
 GTEVKPLQFT NSKLFLFSNG TLYIRNLASS DRGTYECIAT SSTGSERRVV  
 MLTMEEERTS PRIEAASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK  
 AVVDQWSWIH VYPNGSLFIG SVTEKDSGVY LCVARNKMGD DLILMHVSLR  
 LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM  
 QADDGHRTR RYTLFNNGL YFNKVGVAEE GDYTCYAQNT LGKDEMVKHL  
 TVITAAPRIR QSNKTNKRIK AGDTAVLDCE VTGDPKPKIF WLLPSNDMIS  
 FSIDRYTFHA NGSLTINKVK LLDSEGYVCV ARNPSGDDTK MYKLDVVSXP  
 PLINGLYTNR TVIKATAVRH SKKHFDCCRAE GTPSPEVMWI MPDNIFLTAP  
 YYGSRITVHK NGTLEIRNVR LSDSADFICV ARNEGGEESVL VVQLEVLEML  
 RRPTFRNPFN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ  
 SYQYLIASNG SFIISKTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPV

90/90

LTYAPGTVKG ISGESLSLHC VSDGIPKPNI KWTMPSGYVV DRPQINGKYI  
LHDNGTLVIK EATAYDRGNY ICKAQNSVGH TLITVPVMIV AYPPRITNRP  
PRSIVTRTGA AFQLHCVALG VPKPEITWEM PDHSLLSTAS KERTHGSEQL  
HLQGTLVIQN PQTSDSGIYK CTAKNPLGSD YAATYIQVI\*